

## SEQUENCE LISTING

&lt;110&gt; Alibhai, Murtaza

Rydel, Timothy

&lt;120&gt; Insect Inhibitory Lipid Acyl Hydrolases

&lt;130&gt; 38-21 (51842)B

&lt;160&gt; 60

&lt;170&gt; PatentIn version 3.0

&lt;210&gt; 1

&lt;211&gt; 386

&lt;212&gt; PRT

&lt;213&gt; Solanum cardiophyllum

&lt;220&gt;

&lt;221&gt; Protein

&lt;222&gt; (1)..(386)

&lt;223&gt; patatin homolog pat17 amino acid sequence

&lt;400&gt; 1

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Ser Ile Asp Gly Gly Gly Ile Arg Gly Ile Ile Pro Ala Thr Ile Leu
          35           40           45
Glu Phe Leu Glu Gly Gln Leu Gln Glu Met Asp Asn Asn Ala Asp Ala
          50           55           60
Arg Leu Ala Asp Tyr Phe Asp Val Ile Gly Gly Thr Ser Thr Gly Gly
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Leu Leu Thr Ala Met Ile Ser Thr Pro Asn Glu Asn Asn Arg Pro Phe

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Ile	Phe	Asn	Pro	Ser	Gly	Gln	Ile	Leu	Gly	Pro	Lys	Tyr	Asp	Gly	Lys
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Lys	Pro	Val	Ile	Phe	Thr	Lys	Ser	Asn	Leu	Ala	Asn	Ser	Pro	Glu	Leu
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Tyr	Glu	Phe	Asn	Leu	Val	Asp	Gly	Ala	Val	Ala	Thr	Val	Ala	Asp	Pro
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Ala	Leu	Leu	Ser	Ile	Ser	Val	Ala	Thr	Arg	Leu	Ala	Gln	Lys	Asp	Pro
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Ala	Phe	Ala	Ser	Ile	Arg	Ser	Leu	Asn	Tyr	Lys	Lys	Met	Leu	Leu	Leu
				245					250				255		
Ser	Leu	Gly	Thr	Gly	Thr	Thr	Ser	Glu	Phe	Asp	Lys	Thr	Tyr	Thr	Ala
			260					265					270		
Lys	Glu	Ala	Ala	Thr	Trp	Thr	Ala	Val	His	Trp	Met	Leu	Val	Ile	Gln
	275						280					285			
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Thr	Ala	Phe	Gln	Ala	Leu	Asp	Ser	Lys	Asn	Asn	Tyr	Leu	Arg	Val	Gln
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Glu	Asn	Ala	Leu	Thr	Gly	Thr	Thr	Thr	Glu	Met	Asp	Asp	Ala	Ser	Glu
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Ala	Asn	Met	Glu	Leu	Leu	Val	Gln	Val	Gly	Glu	Asn	Leu	Leu	Lys	Lys
			340					345					350		
Pro	Val	Ser	Glu	Asp	Asn	Pro	Glu	Thr	Tyr	Glu	Glu	Ala	Leu	Lys	Arg
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Ser Tyr  
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<210> 2

<211> 365

<212> PRT

<213> synthetic

<220>

<221> Protein

<222> (1)..(365)

<223> Patatin isozyme PatFm (mature protein lacking signal peptide)

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Ile	Lys	Gly	Ile	Ile	Pro	Gly	Thr	Ile	Leu	Glu	Phe	Leu	Glu	Gly	Gln	
			20					25					30			
Leu	Gln	Lys	Met	Asp	Asn	Asn	Ala	Asp	Ala	Arg	Leu	Ala	Asp	Tyr	Phe	
		35					40					45				
Asp	Val	Ile	Gly	Gly	Thr	Ser	Thr	Gly	Gly	Leu	Leu	Thr	Ala	Met	Ile	
	50					55					60					
Thr	Thr	Pro	Asn	Glu	Asn	Asn	Arg	Pro	Phe	Ala	Ala	Ala	Asn	Glu	Ile	
65				70					75						80	
Val	Pro	Phe	Tyr	Phe	Glu	His	Gly	Pro	His	Ile	Phe	Asn	Ser	Arg	Tyr	
				85					90					95		
Trp	Pro	Ile	Phe	Trp	Pro	Lys	Tyr	Asp	Gly	Lys	Tyr	Leu	Met	Gln	Val	
			100					105					110			
Leu	Gln	Glu	Lys	Leu	Gly	Glu	Thr	Arg	Val	His	Gln	Ala	Leu	Thr	Glu	
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Val	Ala	Ile	Ser	Ser	Phe	Asp	Ile	Lys	Thr	Asn	Lys	Pro	Val	Ile	Phe	
	130					135					140					
Thr	Lys	Ser	Asn	Leu	Ala	Lys	Ser	Pro	Glu	Leu	Asp	Ala	Lys	Thr	Tyr	
145				150						155					160	
Asp	Ile	Cys	Tyr	Ser	Thr	Ala	Ala	Ala	Pro	Thr	Tyr	Phe	Pro	Pro	His	
				165					170					175		
Tyr	Phe	Ala	Thr	Asn	Thr	Ile	Asn	Gly	Asp	Lys	Tyr	Glu	Phe	Asn	Leu	
			180					185					190			
Val	Asp	Gly	Ala	Val	Ala	Thr	Val	Ala	Asp	Pro	Ala	Leu	Leu	Ser	Val	
		195					200					205				
Ser	Val	Ala	Thr	Arg	Arg	Ala	Gln	Glu	Asp	Pro	Ala	Phe	Ala	Ser	Ile	
	210					215					220					
Arg	Ser	Leu	Asn	Tyr	Lys	Lys	Met	Leu	Leu	Leu	Ser	Leu	Gly	Thr	Gly	
225				230						235					240	
Thr	Thr	Ser	Glu	Phe	Asp	Lys	Thr	His	Thr	Ala	Glu	Glu	Thr	Ala	Lys	
				245					250					255		
Trp	Gly	Ala	Leu	Gln	Trp	Met	Leu	Val	Ile	Gln	Gln	Met	Thr	Glu	Ala	

260	265	270
Ala Ser Ser Tyr Met Thr Asp Tyr Tyr Leu Ser Thr Val Phe Gln Asp		
275	280	285
Leu His Ser Gln Asn Asn Tyr Leu Arg Val Gln Glu Asn Ala Leu Thr		
290	295	300
Gly Thr Thr Thr Lys Ala Asp Asp Ala Ser Glu Ala Asn Met Glu Leu		
305	310	315
Leu Ala Gln Val Gly Glu Asn Leu Leu Lys Lys Pro Val Ser Lys Asp		
	325	330
Asn Pro Glu Thr Tyr Glu Glu Ala Leu Lys Arg Phe Ala Lys Leu Leu		
	340	345
Ser Asp Arg Lys Lys Leu Arg Ala Asn Lys Ala Ser Tyr		
	355	360
		365

<210> 3

<211> 364

<212> PRT

<213> synthetic

<220>

<221> Protein

<222> (1)..(364)

<223> Patatin isozyme PatIm (mature protein lacking signal peptide)

<400> 3

Pro Trp Leu Glu Glu Met Val Thr Val Leu Ser Ile Asp Gly Gly Gly		
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Ile Lys Gly Ile Ile Pro Ala Ile Ile Leu Glu Phe Leu Glu Gly Gln		
	20	25
Leu Gln Glu Val Asp Asn Asn Lys Asp Ala Arg Leu Ala Asp Tyr Phe		
	35	40
Asp Val Ile Gly Gly Thr Ser Thr Gly Gly Leu Leu Thr Ala Met Ile		
	50	55
Thr Thr Pro Asn Glu Asn Asn Arg Pro Phe Ala Ala Ala Lys Asp Ile		
	65	70
Val Pro Phe Tyr Phe Glu His Gly Pro His Ile Phe Asn Tyr Ser Gly		
	85	90
Ser Ile Leu Gly Pro Met Tyr Asp Gly Lys Tyr Leu Leu Gln Val Leu		
	100	105
Gln Glu Lys Leu Gly Glu Thr Arg Val His Gln Ala Leu Thr Glu Val		
		110

115	120	125
Ala Ile Ser Ser Phe Asp Ile Lys Thr Asn Lys Pro Val Ile Phe Thr 130 135 140		
Lys Ser Asn Leu Ala Lys Ser Pro Glu Leu Asp Ala Lys Met Tyr Asp 145 150 155 160		
Ile Cys Tyr Ser Thr Ala Ala Ala Pro Ile Tyr Phe Pro Pro His His 165 170 175		
Phe Val Thr His Thr Ser Asn Gly Ala Arg Tyr Glu Phe Asn Leu Val 180 185 190		
Asp Gly Ala Val Ala Thr Val Gly Asp Pro Ala Leu Leu Ser Leu Ser 195 200 205		
Val Ala Thr Arg Leu Ala Gln Glu Asp Pro Ala Phe Ser Ser Ile Lys 210 215 220		
Ser Leu Asp Tyr Lys Gln Met Leu Leu Leu Ser Leu Gly Thr Gly Thr 225 230 235 240		
Asn Ser Glu Phe Asp Lys Thr Tyr Thr Ala Glu Glu Ala Ala Lys Trp 245 250 255		
Gly Pro Leu Arg Trp Met Leu Ala Ile Gln Gln Met Thr Asn Ala Ala 260 265 270		
Ser Phe Tyr Met Thr Asp Tyr Tyr Ile Ser Thr Val Phe Gln Ala Arg 275 280 285		
His Ser Gln Asn Asn Tyr Leu Arg Val Gln Glu Asn Ala Leu Asn Gly 290 295 300		
Thr Thr Thr Glu Met Asp Asp Ala Ser Glu Ala Asn Met Glu Leu Leu 305 310 315 320		
Val Gln Val Gly Glu Thr Leu Leu Lys Lys Pro Val Ser Arg Asp Ser 325 330 335		
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<210> 4

<211> 386

<212> PRT

<213> synthetic

<220>

<221> Protein

<222> (1)..(386)

<223> Patatin isozyme PatL+ (including signal peptide)

<400> 4

Met	Ala	Thr	Thr	Lys	Ser	Phe	Leu	Ile	Leu	Phe	Phe	Met	Ile	Leu	Ala	1	5	10	15
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Ser	Ile	Asp	Gly	Gly	Gly	Ile	Lys	Gly	Ile	Ile	Pro	Ala	Ile	Ile	Leu	35	40	45	
Glu	Phe	Leu	Glu	Gly	Gln	Leu	Gln	Glu	Val	Asp	Asn	Asn	Lys	Asp	Ala	50	55	60	
Arg	Leu	Ala	Asp	Tyr	Phe	Asp	Val	Ile	Gly	Gly	Thr	Ser	Thr	Gly	Gly	65	70	75	80
Leu	Leu	Thr	Ala	Met	Ile	Thr	Thr	Pro	Asn	Glu	Asn	Asn	Arg	Pro	Phe	85	90	95	
Ala	Ala	Ala	Lys	Asp	Ile	Val	Pro	Phe	Tyr	Phe	Glu	His	Gly	Pro	His	100	105	110	
Ile	Phe	Asn	Tyr	Ser	Gly	Ser	Ile	Leu	Gly	Pro	Met	Tyr	Asp	Gly	Lys	115	120	125	
Tyr	Leu	Leu	Gln	Val	Leu	Gln	Glu	Lys	Leu	Gly	Glu	Thr	Arg	Val	His	130	135	140	
Gln	Ala	Leu	Thr	Glu	Val	Ala	Ile	Ser	Ser	Phe	Asp	Ile	Lys	Thr	Asn	145	150	155	160
Lys	Pro	Val	Ile	Phe	Thr	Lys	Ser	Asn	Leu	Ala	Lys	Ser	Pro	Glu	Leu	165	170	175	
Asp	Ala	Lys	Met	Tyr	Asp	Ile	Cys	Tyr	Ser	Thr	Ala	Ala	Ala	Pro	Ile	180	185	190	
Tyr	Phe	Pro	Pro	His	His	Phe	Val	Thr	His	Thr	Ser	Asn	Gly	Ala	Arg	195	200	205	
Tyr	Glu	Phe	Asn	Leu	Val	Asp	Gly	Ala	Val	Ala	Thr	Val	Gly	Asp	Pro	210	215	220	
Ala	Leu	Leu	Ser	Leu	Ser	Val	Ala	Thr	Arg	Leu	Ala	Gln	Glu	Asp	Pro	225	230	235	240
Ala	Phe	Ser	Ser	Ile	Lys	Ser	Leu	Asp	Tyr	Lys	Gln	Met	Leu	Leu	Leu	245	250	255	
Ser	Leu	Gly	Thr	Gly	Thr	Asn	Ser	Glu	Phe	Asp	Lys	Thr	Tyr	Thr	Ala	260	265	270	
Glu	Glu	Ala	Ala	Lys	Trp	Gly	Pro	Leu	Arg	Trp	Met	Leu	Ala	Ile	Gln	275	280	285	
Gln	Met	Thr	Asn	Ala	Ala	Ser	Ser	Tyr	Met	Thr	Asp	Tyr	Tyr	Ile	Ser	290	295	300	
Thr	Val	Phe	Gln	Ala	Arg	His	Ser	Gln	Asn	Asn	Tyr	Leu	Arg	Val	Gln	305	310	315	320
Glu	Asn	Ala	Leu	Asn	Gly	Thr	Thr	Thr	Glu	Met	Asp	Asp	Ala	Ser	Glu				

	325		330		335
Ala Asn Met	Glu Leu Leu Val Gln Val Gly Ala Thr Leu Leu Lys Lys				
	340		345		350
Pro Val Ser	Lys Asp Ser Pro Glu Thr Tyr Glu Glu Ala Leu Lys Arg				
	355		360		365
Phe Ala Lys	Leu Leu Ser Asp Arg Lys Lys Leu Arg Ala Asn Lys Ala				
	370		375		380

Ser Tyr  
385

<210> 5

<211> 386

<212> PRT

<213> synthetic

<220>

<221> Protein

<222> (1)..(386)

<223> Patatin isozyme PatA+ (including signal peptide)

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Ser Ile Asp Gly Gly Gly Ile Lys Gly Ile Ile Pro Ala Ile Ile Leu	
	35 40 45
Glu Phe Leu Glu Gly Gln Leu Gln Glu Val Asp Asn Asn Lys Asp Ala	
	50 55 60
Arg Leu Ala Asp Tyr Phe Asp Val Ile Gly Gly Thr Ser Thr Gly Gly	
65	70 75 80
Leu Leu Thr Ala Met Ile Thr Thr Pro Asn Glu Asn Asn Arg Pro Phe	
	85 90 95
Ala Ala Ala Lys Asp Ile Val Pro Phe Tyr Phe Glu His Gly Pro His	
	100 105 110
Ile Phe Asn Tyr Ser Gly Ser Ile Ile Gly Pro Met Tyr Asp Gly Lys	
	115 120 125
Tyr Leu Leu Gln Val Leu Gln Glu Lys Leu Gly Glu Thr Arg Val His	
	130 135 140
Gln Ala Leu Thr Glu Val Ala Ile Ser Ser Phe Asp Ile Lys Thr Asn	

145		150		155		160									
Lys	Pro	Val	Ile	Phe	Thr	Lys	Ser	Asn	Leu	Ala	Lys	Ser	Pro	Glu	Leu
				165					170					175	
Asp	Ala	Lys	Met	Tyr	Asp	Ile	Cys	Tyr	Ser	Thr	Ala	Ala	Ala	Pro	Ile
			180					185					190		
Tyr	Phe	Pro	Pro	His	Tyr	Phe	Ile	Thr	His	Thr	Ser	Asn	Gly	Asp	Ile
		195					200					205			
Tyr	Glu	Phe	Asn	Leu	Val	Asp	Gly	Gly	Val	Ala	Thr	Val	Gly	Asp	Pro
	210					215					220				
Ala	Leu	Leu	Ser	Leu	Ser	Val	Ala	Thr	Arg	Leu	Ala	Gln	Glu	Asp	Pro
225					230					235					240
Ala	Phe	Ser	Ser	Ile	Lys	Ser	Leu	Asp	Tyr	Lys	Gln	Met	Leu	Leu	Leu
				245					250					255	
Ser	Leu	Gly	Thr	Gly	Thr	Asn	Ser	Glu	Phe	Asp	Lys	Thr	Tyr	Thr	Ala
			260					265					270		
Gln	Glu	Ala	Ala	Lys	Trp	Gly	Pro	Leu	Arg	Trp	Met	Leu	Ala	Ile	Gln
		275					280					285			
Gln	Met	Thr	Asn	Ala	Ala	Ser	Ser	Tyr	Met	Thr	Asp	Tyr	Tyr	Ile	Ser
	290					295					300				
Thr	Val	Phe	Gln	Ala	Arg	His	Ser	Gln	Asn	Asn	Tyr	Leu	Arg	Val	Gln
305					310					315					320
Glu	Asn	Ala	Leu	Thr	Gly	Thr	Thr	Thr	Glu	Met	Asp	Asp	Ala	Ser	Glu
				325					330					335	
Ala	Asn	Met	Glu	Leu	Leu	Val	Gln	Val	Gly	Glu	Thr	Leu	Leu	Lys	Lys
			340					345					350		
Pro	Val	Ser	Lys	Asp	Ser	Pro	Glu	Thr	Tyr	Glu	Glu	Ala	Leu	Lys	Arg
		355					360					365			
Phe	Ala	Lys	Leu	Leu	Ser	Asp	Arg	Lys	Lys	Leu	Arg	Ala	Asn	Lys	Ala
	370					375					380				

Ser Tyr  
385

<210> 6

<211> 386

<212> PRT

<213> synthetic

<220>

<221> Protein

<222> (1)..(386)

<223> Patatin isozyme PatB+ (including signal peptide)



<400> 6

Met	Ala	Thr	Thr	Lys	Ser	Val	Leu	Val	Leu	Phe	Phe	Met	Ile	Leu	Ala
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Thr	Thr	Ser	Ser	Thr	Cys	Ala	Thr	Leu	Gly	Glu	Met	Val	Thr	Val	Leu
			20					25					30		
Ser	Ile	Asp	Gly	Gly	Gly	Ile	Lys	Gly	Ile	Ile	Pro	Ala	Thr	Ile	Leu
		35					40					45			
Glu	Phe	Leu	Glu	Gly	Gln	Leu	Gln	Glu	Val	Asp	Asn	Asn	Lys	Asp	Ala
	50					55					60				
Arg	Leu	Ala	Asp	Tyr	Phe	Asp	Val	Ile	Gly	Gly	Thr	Ser	Thr	Gly	Gly
65					70				75						80
Leu	Leu	Thr	Ala	Met	Ile	Thr	Thr	Pro	Asn	Glu	Asn	Asn	Arg	Pro	Phe
				85					90					95	
Ala	Ala	Ala	Lys	Asp	Ile	Val	Pro	Phe	Tyr	Phe	Glu	His	Gly	Pro	His
			100					105					110		
Ile	Phe	Asn	Ser	Ser	Gly	Ser	Ile	Phe	Gly	Pro	Met	Tyr	Asp	Gly	Lys
		115					120					125			
Tyr	Phe	Leu	Gln	Val	Leu	Gln	Glu	Lys	Leu	Gly	Glu	Thr	Arg	Val	His
	130					135					140				
Gln	Ala	Leu	Thr	Glu	Val	Ala	Ile	Ser	Ser	Phe	Asp	Ile	Lys	Thr	Asn
145					150					155					160
Lys	Pro	Val	Ile	Phe	Thr	Lys	Ser	Asn	Leu	Ala	Lys	Ser	Pro	Glu	Leu
				165					170					175	
Asp	Ala	Lys	Met	Asn	Asp	Ile	Cys	Tyr	Ser	Thr	Ala	Ala	Ala	Pro	Thr
			180					185					190		
Tyr	Phe	Pro	Pro	His	Tyr	Phe	Val	Thr	His	Thr	Ser	Asn	Gly	Asp	Lys
		195					200					205			
Tyr	Glu	Phe	Asn	Leu	Val	Asp	Gly	Ala	Val	Ala	Thr	Val	Gly	Asp	Pro
	210					215					220				
Ala	Leu	Leu	Ser	Leu	Ser	Val	Arg	Thr	Lys	Leu	Ala	Gln	Val	Asp	Pro
225					230					235					240
Lys	Phe	Ala	Ser	Ile	Lys	Ser	Leu	Asn	Tyr	Asn	Glu	Met	Leu	Leu	Leu
				245					250				255		
Ser	Leu	Gly	Thr	Gly	Thr	Asn	Ser	Glu	Phe	Asp	Lys	Thr	Tyr	Thr	Ala
			260					265					270		
Glu	Glu	Ala	Ala	Lys	Trp	Gly	Pro	Leu	Arg	Trp	Ile	Leu	Ala	Ile	Gln
		275					280					285			
Gln	Met	Thr	Asn	Ala	Ala	Ser	Ser	Tyr	Met	Thr	Asp	Tyr	Tyr	Leu	Ser
	290					295					300				
Thr	Val	Phe	Gln	Ala	Arg	His	Ser	Gln	Asn	Asn	Tyr	Leu	Arg	Val	Gln
305					310					315					320
Glu	Asn	Ala	Leu	Thr	Gly	Thr	Thr	Thr	Glu	Met	Asp	Asp	Ala	Ser	Glu

	325		330		335
Ala Asn Met	Glu Leu Leu Val Gln Val Gly Glu Lys Leu Leu Lys Lys				
	340		345		350
Pro Val Ser	Lys Asp Ser Pro Glu Thr Tyr Glu Glu Ala Leu Lys Arg				
	355		360		365
Phe Ala Lys	Leu Leu Ser Asp Arg Lys Lys Leu Arg Ala Asn Lys Ala				
	370		375		380

Ser Tyr  
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<210> 7

<211> 408

<212> PRT

<213> Pentaclethra macroloba

<220>

<221> Protein

<222> (1)..(408)

<223> patatin homolog pentin 1

<400> 7

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Gly Asn Leu Val	Thr Val Leu Ala Ile Asp Gly Gly Gly Ile Arg Gly
	35 40 45
Ile Ile Pro Gly	Val Ile Leu Lys Gln Leu Glu Ala Thr Leu Gln Arg
	50 55 60
Trp Asp Ser Ser	Ala Arg Leu Ala Glu Tyr Phe Asp Val Val Ala Gly
65	70 75 80
Thr Ser Thr Gly	Gly Ile Ile Thr Ala Ile Leu Thr Ala Pro Asp Pro
	85 90 95
Gln Asn Lys Asp	Arg Pro Leu Tyr Ala Ala Glu Glu Ile Ile Asp Phe
	100 105 110
Tyr Ile Glu His	Gly Pro Ser Ile Phe Asn Lys Ser Thr Ala Cys Ser
	115 120 125
Leu Pro Gly Ile	Phe Cys Pro Lys Tyr Asp Gly Lys Tyr Leu Gln Glu
	130 135 140
Ile Ile Ser Gln	Lys Leu Asn Glu Thr Leu Leu Asp Gln Thr Thr Thr

145	150	155	160
Asn Val Val Ile Pro Ser Phe Asp Ile Lys Leu Leu Arg Pro Thr Ile	165	170	175
Phe Ser Thr Phe Lys Leu Glu Glu Val Pro Glu Leu Asn Val Lys Leu	180	185	190
Ser Asp Val Cys Met Gly Thr Ser Ala Ala Pro Ile Val Phe Pro Pro	195	200	205
Tyr Tyr Phe Lys His Gly Asp Thr Glu Phe Asn Leu Val Asp Gly Ala	210	215	220
Ile Ile Ala Asp Ile Pro Ala Pro Val Ala Leu Ser Glu Val Leu Gln	225	230	235
Gln Glu Lys Tyr Lys Asn Lys Glu Ile Leu Leu Leu Ser Ile Gly Thr	245	250	255
Gly Val Val Lys Pro Gly Glu Gly Tyr Ser Ala Asn Arg Thr Trp Thr	260	265	270
Ile Phe Asp Trp Ser Ser Glu Thr Leu Ile Gly Leu Met Gly His Gly	275	280	285
Thr Arg Ala Met Ser Asp Tyr Tyr Val Gly Ser His Phe Lys Ala Leu	290	295	300
Gln Pro Gln Asn Asn Tyr Leu Arg Ile Gln Glu Tyr Asp Leu Asp Pro	305	310	315
Ala Leu Glu Ser Ile Asp Asp Ala Ser Thr Glu Asn Met Glu Asn Leu	325	330	335
Glu Lys Val Gly Gln Ser Leu Leu Asn Glu Pro Val Lys Arg Met Asn	340	345	350
Leu Asn Thr Phe Val Val Glu Glu Thr Gly Glu Gly Thr Asn Ala Glu	355	360	365
Ala Leu Asp Arg Leu Ala Gln Ile Leu Tyr Glu Glu Lys Ile Thr Arg	370	375	380
Gly Leu Gly Lys Ile Ser Leu Glu Val Asp Asn Ile Asp Pro Tyr Thr	385	390	395
Glu Arg Val Arg Lys Leu Leu Phe	405		

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<212> PRT

<213> Zea mays

<220>

<221> Protein

<222> (1)..(410)

<223> monocot patatin homolog 5c9

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Pro	Pro	Pro	Ser	Thr	Gly	Lys	Leu	Ile	Thr	Ile	Leu	Ser	Ile	Asp	Gly	
			20					25					30			
Gly	Gly	Ile	Arg	Gly	Leu	Ile	Pro	Ala	Thr	Ile	Ile	Ala	Tyr	Leu	Glu	
		35					40					45				
Ala	Lys	Leu	Gln	Glu	Leu	Asp	Gly	Pro	Asp	Ala	Arg	Ile	Ala	Asp	Tyr	
	50					55					60					
Phe	Asp	Val	Ile	Ala	Gly	Thr	Ser	Thr	Gly	Ala	Leu	Leu	Ala	Ser	Met	
65					70					75					80	
Leu	Ala	Ala	Pro	Asp	Glu	Asn	Asn	Arg	Pro	Leu	Phe	Ala	Ala	Lys	Asp	
				85					90					95		
Leu	Thr	Thr	Phe	Tyr	Leu	Glu	Asn	Gly	Pro	Lys	Ile	Phe	Pro	Gln	Lys	
			100					105					110			
Lys	Ala	Gly	Leu	Leu	Thr	Pro	Leu	Arg	Asn	Leu	Leu	Gly	Leu	Val	Arg	
		115					120					125				
Gly	Pro	Lys	Tyr	Asp	Gly	Val	Phe	Leu	His	Asp	Lys	Ile	Lys	Ser	Leu	
	130					135					140					
Thr	His	Asp	Val	Arg	Val	Ala	Asp	Thr	Val	Thr	Asn	Val	Ile	Val	Pro	
145					150					155					160	
Ala	Phe	Asp	Val	Lys	Tyr	Leu	Gln	Pro	Ile	Ile	Phe	Ser	Thr	Tyr	Glu	
				165					170					175		
Ala	Lys	Thr	Asp	Thr	Leu	Lys	Asn	Ala	His	Leu	Ser	Asp	Ile	Cys	Ile	
			180					185					190			
Ser	Thr	Ser	Ala	Ala	Pro	Thr	Tyr	Phe	Pro	Ala	His	Phe	Phe	Lys	Thr	
		195					200					205				
Glu	Ala	Thr	Asp	Gly	Arg	Pro	Pro	Arg	Glu	Tyr	His	Leu	Val	Asp	Gly	
	210					215					220					
Gly	Val	Ala	Ala	Asn	Asn	Pro	Thr	Met	Val	Ala	Met	Ser	Met	Leu	Thr	
225					230					235					240	
Lys	Glu	Val	His	Arg	Arg	Asn	Pro	Asn	Phe	Asn	Ala	Gly	Ser	Pro	Thr	
				245					250					255		
Glu	Tyr	Thr	Asn	Tyr	Leu	Ile	Ile	Ser	Val	Gly	Thr	Gly	Ser	Ala	Lys	
			260					265					270			
Gln	Ala	Glu	Lys	Tyr	Thr	Ala	Glu	Gln	Cys	Ala	Lys	Trp	Gly	Leu	Ile	
		275					280					285				
Gln	Trp	Leu	Tyr	Asn	Gly	Gly	Phe	Thr	Pro	Ile	Ile	Asp	Ile	Phe	Ser	
	290					295					300					
His	Ala	Ser	Ser	Asp	Met	Val	Asp	Ile	His	Ala	Ser	Ile	Leu	Phe	Gln	

305		310		315		320
Ala Leu His Cys Glu Lys Lys Tyr Leu Arg Ile Gln Asp Asp Thr Leu	325			330		335
Thr Gly Asn Ala Ser Ser Val Asp Ile Ala Thr Lys Glu Asn Met Glu	340		345			350
Ser Leu Ile Ser Ile Gly Gln Glu Leu Leu Lys Lys Pro Val Ala Arg	355		360			365
Val Asn Ile Asp Thr Gly Val Tyr Glu Ser Cys Asp Gly Glu Gly Thr	370		375		380	
Asn Ala Gln Ser Leu Ala Asp Phe Ala Lys Gln Leu Ser Asp Glu Arg	385	390		395		400
Lys Leu Arg Lys Ser Asn Leu Asn Ser Asn	405		410			

<210> 9

<211> 508

<212> PRT

<213> synthetic

<220>

<221> Protein

<222> (1)..(508)

<223> maize patatin homolog amino acid sequence corn 1

<400> 9

Arg Pro Thr Arg Pro Arg His Pro Arg Asn Thr Gln Lys Arg Gly Ala	1	5		10		15
Leu Leu Val Gly Trp Ile Leu Phe Ser Leu Ala Ala Ser Pro Val Lys	20		25			30
Phe Gln Thr His Met Gly Ser Ile Gly Arg Gly Thr Ala Asn Cys Ala	35		40		45	
Thr Val Pro Gln Pro Pro Pro Ser Thr Gly Lys Leu Ile Thr Ile Leu	50		55		60	
Ser Ile Asp Gly Gly Gly Ile Arg Gly Leu Ile Pro Ala Thr Ile Ile	65		70		75	80
Ala Tyr Leu Glu Ala Lys Leu Gln Glu Leu Asp Gly Pro Asp Ala Arg	85		90			95
Ile Ala Asp Tyr Phe Asp Val Ile Ala Gly Thr Ser Thr Gly Ala Leu	100		105		110	
Leu Ala Ser Met Leu Ala Ala Pro Asp Glu Asn Asn Arg Pro Leu Phe						

115					120					125					
Ala	Ala	Lys	Asp	Leu	Thr	Thr	Phe	Tyr	Leu	Glu	Asn	Gly	Pro	Lys	Ile
130						135					140				
Phe	Pro	Gln	Lys	Lys	Ala	Gly	Leu	Leu	Thr	Pro	Leu	Arg	Asn	Leu	Leu
145				150						155					160
Gly	Leu	Val	Arg	Gly	Pro	Lys	Tyr	Asp	Gly	Val	Phe	Leu	His	Asp	Lys
				165					170					175	
Ile	Lys	Ser	Leu	Thr	His	Asp	Val	Arg	Val	Ala	Asp	Thr	Val	Thr	Asn
			180					185					190		
Val	Ile	Val	Pro	Ala	Phe	Asp	Val	Lys	Tyr	Leu	Gln	Pro	Ile	Ile	Phe
		195					200					205			
Ser	Thr	Tyr	Glu	Ala	Lys	Thr	Asp	Ala	Leu	Lys	Asn	Ala	His	Leu	Ser
	210					215					220				
Asp	Ile	Cys	Ile	Ser	Thr	Ser	Ala	Ala	Pro	Thr	Tyr	Phe	Pro	Ala	His
225					230					235					240
Phe	Phe	Lys	Thr	Glu	Ala	Thr	Asp	Gly	Arg	Pro	Pro	Arg	Glu	Tyr	His
				245					250					255	
Leu	Val	Asp	Gly	Gly	Val	Ala	Ala	Asn	Asn	Pro	Thr	Met	Val	Ala	Met
			260					265					270		
Ser	Met	Leu	Thr	Lys	Glu	Val	His	Arg	Arg	Asn	Pro	Asn	Phe	Asn	Ala
		275					280					285			
Gly	Ser	Pro	Thr	Glu	Tyr	Thr	Asn	Tyr	Leu	Ile	Ile	Ser	Val	Gly	Thr
	290					295					300				
Gly	Ser	Ala	Lys	Gln	Ala	Glu	Lys	Tyr	Thr	Ala	Glu	Gln	Cys	Ala	Lys
305				310						315					320
Trp	Gly	Leu	Ile	Gln	Trp	Leu	Tyr	Asn	Gly	Gly	Phe	Thr	Pro	Ile	Ile
				325					330					335	
Asp	Ile	Phe	Ser	His	Ala	Ser	Ser	Asp	Met	Val	Asp	Ile	His	Ala	Ser
			340					345					350		
Ile	Leu	Phe	Gln	Ala	Leu	His	Cys	Glu	Lys	Lys	Tyr	Leu	Arg	Ile	Gln
		355					360					365			
Leu	Tyr	Tyr	Ala	Gly	Tyr	Phe	Asp	Trp	Glu	Arg	Ile	Val	Arg	Gly	His
	370					375					380				
Arg	His	Gln	Gly	Glu	His	Gly	Val	Ser	Asp	Ile	Asp	Arg	Pro	Gly	Ala
385				390						395					400
Ala	Gln	Glu	Ala	Ser	Gly	Glu	Ser	Glu	His	Arg	His	Arg	Ala	Val	Arg
				405					410					415	
Val	Leu	Arg	Arg	Gly	His	Lys	Cys	Thr	Val	Ala	Ser	Leu	Arg	Gln	Ala
			420					425					430		
Thr	Leu	Arg	Ala	Gln	Ala	Thr	Gln	Glu	Gln	Ser	Gln	Leu	Gln	Leu	Ile
		435					440					445			
Asn	Thr	Ser	Leu	Ser	His	Ser	Met	Cys	Ser	Phe	Arg	Arg	Phe	Thr	Val
	450					455					460				
Ser	Tyr	Phe	Phe	Asn	Phe	Asn	Ser	Val	Cys	Val	Leu	Cys	Val	Leu	Cys

465                      470                      475                      480  
 Val Tyr Gln Thr Phe Lys Phe Asn Gln Lys Lys Lys Lys Lys Lys Lys  
                                  485                                   490                                   495

Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Arg Ala Ala  
                                  500                                   505

<210> 10

<211> 410

<212> PRT

<213> synthetic

<220>

<221> Protein

<222> (1)..(410)

<223> maize patatin homolog amino acid sequence corn 2

<400> 10

Met Gly Ser Ile Gly Arg Gly Thr Ala Asn Cys Ala Thr Val Pro Gln  
 1                      5                      10                      15

Pro Pro Pro Ser Thr Gly Lys Leu Ile Thr Ile Leu Ser Ile Asp Gly  
                                  20                      25                      30

Gly Gly Ile Arg Gly Leu Ile Pro Ala Thr Ile Ile Ala Tyr Leu Glu  
                                  35                      40                      45

Ala Lys Leu Gln Glu Leu Asp Gly Pro Asp Ala Arg Ile Ala Asp Tyr  
                                  50                      55                      60

Phe Asp Val Ile Ala Gly Thr Ser Thr Gly Ala Leu Leu Ala Ser Met  
 65                      70                      75                      80

Leu Ala Ala Pro Asp Glu Asn Asn Arg Pro Leu Phe Ala Ala Lys Asp  
                                  85                      90                      95

Leu Thr Thr Phe Tyr Leu Glu Asn Gly Pro Lys Ile Phe Pro Gln Lys  
                                  100                      105                      110

Lys Ala Gly Leu Leu Thr Pro Leu Arg Asn Leu Leu Gly Leu Val Arg  
                                  115                      120                      125

Gly Pro Lys Tyr Asp Gly Val Phe Leu His Asp Lys Ile Lys Ser Leu  
                                  130                      135                      140

Thr His Asp Val Arg Val Ala Asp Thr Val Thr Asn Val Ile Val Pro  
 145                      150                      155                      160

Ala Phe Asp Val Lys Ser Leu Gln Pro Ile Ile Phe Ser Thr Tyr Glu  
                                  165                      170                      175

Ala Lys Thr Asp Thr Leu Lys Asn Ala His Leu Ser Asp Ile Cys Ile





<400> 11

Met	Gly	Ser	Ile	Gly	Arg	Gly	Thr	Ala	Asn	Cys	Ala	Thr	Val	Pro	Gln	1	5	10	15
Pro	Pro	Pro	Ser	Thr	Gly	Lys	Leu	Ile	Thr	Ile	Leu	Ser	Ile	Asp	Gly	20	25	30	
Gly	Gly	Ile	Arg	Gly	Leu	Ile	Pro	Ala	Thr	Ile	Ile	Ala	Tyr	Leu	Glu	35	40	45	
Ala	Lys	Leu	Gln	Glu	Leu	Asp	Gly	Pro	Asp	Ala	Arg	Ile	Ala	Asp	Tyr	50	55	60	
Phe	Asp	Val	Ile	Ala	Gly	Thr	Ser	Thr	Gly	Ala	Leu	Leu	Ala	Ser	Met	65	70	75	80
Leu	Ala	Ala	Pro	Asp	Glu	Asn	Asn	Arg	Pro	Leu	Phe	Ala	Ala	Lys	Asp	85	90	95	
Leu	Thr	Thr	Phe	Tyr	Leu	Glu	Asn	Gly	Pro	Lys	Ile	Phe	Pro	Gln	Lys	100	105	110	
Lys	Ala	Gly	Leu	Leu	Thr	Pro	Leu	Arg	Asn	Leu	Leu	Gly	Leu	Val	Arg	115	120	125	
Gly	Pro	Lys	Tyr	Asp	Gly	Val	Phe	Leu	His	Asp	Lys	Ile	Lys	Ser	Leu	130	135	140	
Thr	His	Asp	Val	Arg	Val	Ala	Asp	Thr	Val	Thr	Asn	Val	Ile	Val	Pro	145	150	155	160
Ala	Phe	Asp	Val	Lys	Tyr	Leu	Gln	Pro	Ile	Ile	Phe	Ser	Thr	Tyr	Glu	165	170	175	
Ala	Lys	Thr	Asp	Ala	Leu	Lys	Asn	Ala	His	Leu	Ser	Asp	Ile	Cys	Ile	180	185	190	
Ser	Thr	Ser	Ala	Ala	Pro	Thr	Tyr	Phe	Pro	Ala	His	Phe	Phe	Lys	Thr	195	200	205	
Glu	Ala	Thr	Asp	Gly	Arg	Pro	Pro	Arg	Glu	Tyr	His	Leu	Val	Asp	Gly	210	215	220	
Gly	Val	Ala	Ala	Asn	Asn	Pro	Thr	Met	Val	Ala	Met	Ser	Met	Leu	Thr	225	230	235	240
Lys	Glu	Val	His	Arg	Arg	Asn	Pro	Asn	Phe	Asn	Ala	Gly	Ser	Pro	Thr	245	250	255	
Glu	Tyr	Thr	Asn	Tyr	Leu	Ile	Ile	Ser	Val	Gly	Thr	Gly	Ser	Ala	Lys	260	265	270	
Gln	Ala	Glu	Lys	Tyr	Thr	Ala	Glu	Gln	Cys	Ala	Lys	Trp	Gly	Leu	Ile	275	280	285	
Gln	Trp	Leu	Tyr	Asn	Gly	Gly	Phe	Thr	Pro	Ile	Ile	Asp	Ile	Phe	Ser	290	295	300	
His	Ala	Ser	Ser	Asp	Met	Val	Asp	Ile	His	Ala	Ser	Ile	Leu	Phe	Gln	305	310	315	320
Ala	Leu	His	Cys	Glu	Lys	Lys	Tyr	Leu	Arg	Ile	Gln	Asp	Asp	Thr	Leu	325	330	335	
Thr	Gly	Asn	Ala	Ser	Ser	Val	Asp	Ile	Ala	Thr	Lys	Glu	Asn	Met	Glu				

340	345	350
Ser Leu Ile Ser Ile Gly Gln Glu Leu Leu Lys Lys Pro Val Ala Arg		
355	360	365
Val Asn Ile Asp Thr Gly Leu Tyr Glu Ser Cys Asp Gly Glu Gly Thr		
370	375	380
Asn Ala Gln Ser Leu Ala Asp Phe Ala Lys Gln Leu Ser Asp Glu Arg		
385	390	395
Lys Leu Arg Lys Ser Asn Leu Asn Ser Asn		
405	410	

<210> 12

<211> 410

<212> PRT

<213> synthetic

<220>

<221> Protein

<222> (1)..(410)

<223> maize patatin homolog amino acid sequence corn 4

<400> 12

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20	30
Gly Gly Ile Arg Gly Leu Ile Pro Ala Thr Ile Ile Ala Tyr Leu Glu	
35	45
Ala Lys Leu Gln Glu Leu Asp Gly Pro Asp Ala Arg Ile Ala Asp Tyr	
50	60
Phe Asp Val Ile Ala Gly Thr Ser Thr Gly Ala Leu Leu Ala Ser Met	
65	75
Leu Ala Ala Pro Asp Glu Asn Asn Arg Pro Leu Phe Ala Ala Lys Asp	
85	95
Leu Thr Thr Phe Tyr Leu Glu Asn Gly Pro Lys Ile Phe Pro Gln Lys	
100	110
Lys Ala Gly Leu Leu Thr Pro Leu Arg Asn Leu Leu Gly Leu Val Arg	
115	125
Gly Pro Lys Tyr Asp Gly Val Phe Leu His Asp Lys Ile Lys Ser Leu	
130	140
Thr His Asp Val Arg Val Ala Asp Thr Val Thr Asn Val Ile Val Pro	

145		150		155		160
Ala Phe Asp Val	Lys Ser Leu Gln Pro	Ile Ile Phe Ser Thr	Tyr Glu			
	165		170			175
Ala Lys Thr Asp Thr	Leu Lys Asn Ala His	Leu Ser Asp Ile	Cys Ile			
	180		185			190
Ser Thr Ser Ala Ala	Pro Thr Tyr Phe Pro	Ala His Phe Phe	Lys Ile			
	195		200			205
Glu Ala Thr Asp Gly	Arg Pro Pro Arg	Glu Tyr His Leu	Val Asp Gly			
	210		215			220
Gly Val Ala Ala Asn	Asn Pro Thr Met Val	Ala Met Ser Met	Leu Thr			
	225		230			235
Lys Glu Val His Arg	Arg Asn Pro Asn Phe	Asn Ala Gly Ser	Pro Thr			
	245		250			255
Glu Tyr Thr Asn Tyr	Leu Ile Ile Ser Val	Gly Thr Gly Ser	Ala Lys			
	260		265			270
Gln Ala Glu Lys Tyr	Thr Ala Glu Gln Cys	Ala Lys Trp Gly	Leu Ile			
	275		280			285
Gln Trp Leu Tyr Asn	Gly Gly Phe Thr Pro	Ile Ile Asp Ile	Phe Ser			
	290		295			300
His Ala Ser Ser Asp	Met Val Asp Ile His	Ala Ser Ile Leu	Phe Gln			
	305		310			315
Ala Leu His Cys Glu	Lys Lys Tyr Leu Arg	Ile Gln Asp Asp	Thr Leu			
	325		330			335
Thr Gly Asn Ala Ser	Ser Val Asp Ile Ala	Thr Lys Glu Asn	Met Glu			
	340		345			350
Ser Leu Ile Ser Ile	Gly Gln Glu Leu Leu	Asn Lys Pro Val	Ala Arg			
	355		360			365
Val Asn Ile Asp Thr	Gly Leu Tyr Glu Ser	Cys Glu Gly Glu	Gly Thr			
	370		375			380
Asn Ala Gln Ser Leu	Ala Asp Phe Ala Lys	Gln Leu Ser Asp	Glu Arg			
	385		390			395
Lys Leu Arg Lys Ser	Asn Leu Asn Ser Asn					
	405		410			

<210> 13

<211> 337

<212> PRT

<213> synthetic

<220>

<221> Protein

<222> (1)..(337)

<223> maize patatin homolog amino acid sequence corn 5

<400> 13

Met	Gly	Ser	Ile	Gly	Arg	Gly	Thr	Ala	Asn	Cys	Ala	Thr	Val	Pro	Gln	1	5	10	15
Pro	Pro	Pro	Ser	Thr	Gly	Lys	Leu	Ile	Thr	Ile	Leu	Ser	Ile	Asp	Gly	20	25	30	
Gly	Gly	Ile	Arg	Gly	Leu	Ile	Pro	Ala	Thr	Ile	Ile	Ala	Tyr	Leu	Glu	35	40	45	
Ala	Lys	Leu	Gln	Glu	Leu	Asp	Gly	Pro	Asp	Ala	Arg	Ile	Ala	Asp	Tyr	50	55	60	
Phe	Asp	Val	Ile	Ala	Gly	Thr	Ser	Thr	Gly	Ala	Leu	Leu	Ala	Ser	Met	65	70	75	80
Leu	Ala	Ala	Pro	Asp	Glu	Asn	Asn	Arg	Pro	Leu	Phe	Ala	Ala	Lys	Asp	85	90	95	
Leu	Thr	Thr	Phe	Tyr	Leu	Glu	Asn	Gly	Pro	Lys	Ile	Phe	Pro	Gln	Lys	100	105	110	
Lys	Ala	Gly	Leu	Leu	Thr	Pro	Leu	Arg	Asn	Leu	Leu	Gly	Leu	Val	Arg	115	120	125	
Gly	Pro	Lys	Tyr	Asp	Gly	Val	Phe	Leu	His	Asp	Lys	Ile	Lys	Ser	Leu	130	135	140	
Thr	His	Asp	Val	Arg	Val	Ala	Asp	Thr	Val	Thr	Asn	Val	Ile	Val	Pro	145	150	155	160
Ala	Phe	Asp	Val	Lys	Tyr	Leu	Gln	Pro	Ile	Ile	Phe	Ser	Thr	Tyr	Glu	165	170	175	
Ala	Lys	Thr	Asp	Ala	Leu	Lys	Asn	Ala	His	Leu	Ser	Asp	Ile	Cys	Ile	180	185	190	
Ser	Thr	Ser	Ala	Ala	Pro	Thr	Tyr	Phe	Pro	Ala	His	Phe	Phe	Lys	Thr	195	200	205	
Glu	Ala	Thr	Asp	Gly	Arg	Pro	Pro	Arg	Glu	Tyr	His	Leu	Val	Asp	Gly	210	215	220	
Gly	Val	Ala	Ala	Asn	Asn	Pro	Thr	Met	Val	Ala	Met	Ser	Met	Leu	Thr	225	230	235	240
Lys	Glu	Val	His	Arg	Arg	Asn	Pro	Asn	Phe	Asn	Ala	Gly	Ser	Pro	Thr	245	250	255	
Glu	Tyr	Thr	Asn	Tyr	Leu	Ile	Ile	Ser	Val	Gly	Thr	Gly	Ser	Ala	Lys	260	265	270	
Gln	Ala	Glu	Lys	Tyr	Thr	Ala	Glu	Gln	Cys	Ala	Lys	Trp	Gly	Leu	Ile	275	280	285	
Gln	Trp	Leu	Tyr	Asn	Gly	Gly	Phe	Thr	Pro	Ile	Ile	Asp	Ile	Phe	Ser	290	295	300	
His	Ala	Ser	Ser	Asp	Met	Val	Asp	Ile	His	Ala	Ser	Ile	Leu	Phe	Gln				



<212> PRT

<213> synthetic

<220>

<221> Protein

<222> (1)..(3)

<223> Linker Sequence

<400> 16

Gly Pro Gly  
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<210> 17

<211> 7

<212> PRT

<213> synthetic

<220>

<221> Protein

<222> (1)..(7)

<223> Linker Sequence 2

<400> 17

Gly Gly Gly Ser Gly Gly Gly  
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<210> 18

<211> 33

<212> DNA

<213> synthetic

<220>

<221> DNA

<222> (1)..(33)

<223> oligonucleotide-1

<400> 18  
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33

<210> 19

<211> 33

<212> DNA

<213> synthetic

<220>

<221> DNA

<222> (1)..(33)

<223> oligonucleotide-2

<400> 19  
ccagaattct cattaataag aagctttggt tgc

33

<210> 20

<211> 1128

<212> DNA

<213> synthetic

<220>

<221> DNA

<222> (1)..(1128)

<223> pMON37402 sequence encoding permutein protein

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gcactggcac tacttcagag ttgataaaa catatacagc aaaagaggca gctacctgga 120  
ctgctgtaca ttggatgtta gttatacaga aaatgactga tgcagcaagt tcttacatga 180  
ctgattatta cctttctact gcttttcaag ctcttgattc aaaaaacaat tacctcaggg 240

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ttcaagaaaa tgcattaaca ggcacaacta ctgaaatgga tgatgcttct gaggctaata 300
tggaattatt agtacaagtt ggtgaaaact tattgaagaa accagtttcc gaagacaatc 360
ctgaaaccta tgaggaagct ctaaagaggt ttgcaaaatt gctctctgat aggaagaaac 420
tccgagcaaa caaagcttct tatggaccag gacagttggg agaaatgggtg actgttctta 480
gtattgatgg aggtggaatt agagggatca ttccggctac cattctcgaa tttcttgaag 540
gacaacttca ggaaatggac aataatgcag atgcaagact tgcagattac tttgatgtaa 600
ttggaggaac aagtacagga ggtttattga ctgctatgat aagtactcca aatgaaaaca 660
atcgaccctt tgctgctgcc aaagaaattg taccttttta cttcgaacat ggccctcaga 720
tttttaatcc tagtgggtcaa attttaggcc caaaatatga tggaaaatat cttatgcaag 780
ttcttcaaga aaaacttgga gaaactcgtg tgcatcaagc tttgacagaa gttgtcatct 840
caagctttga catcaaaaaca aataagccag taatattcac taagtcaaat ttagcaaact 900
ctccagaatt ggatgctaag atgtatgaca taagttattc cacagcagca gctccaacat 960
atcttctccc gcattacttt gttactaata ctagtaatgg agatgaatat gagttcaatc 1020
ttgttgatgg tgctgttgct actgttgctg atccggcggtt attatccatt agcgttgcaa 1080
cgagacttgc acaaaaggat ccagcatttg cttcaattag gtaatgag 1128

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<210> 21

<211> 366

<212> PRT

<213> synthetic

<220>

<221> Protein

<222> (1)..(366)

<223> Permutin protein encoded from pMON37402 sequence

<400> 21

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Ser Leu Asn Tyr Lys Lys Met Leu Leu Leu Ser Leu Gly Thr Gly Thr
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Thr Ser Glu Phe Asp Lys Thr Tyr Thr Ala Lys Glu Ala Ala Thr Trp
          20           25           30

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Thr Ala Val His Trp Met Leu Val Ile Gln Lys Met Thr Asp Ala Ala
          35           40           45

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Ser Ser Tyr Met Thr Asp Tyr Tyr Leu Ser Thr Ala Phe Gln Ala Leu

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50					55					60					
Asp 65	Ser	Lys	Asn	Asn 70	Tyr	Leu	Arg	Val	Gln	Glu 75	Asn	Ala	Leu	Thr	Gly 80
Thr	Thr	Thr	Glu	Met 85	Asp	Asp	Ala	Ser	Glu 90	Ala	Asn	Met	Glu	Leu	Leu 95
Val	Gln	Val	Gly 100	Glu	Asn	Leu	Leu	Lys 105	Lys	Pro	Val	Ser	Glu	Asp	Asn 110
Pro	Glu	Thr 115	Tyr	Glu	Glu	Ala	Leu	Lys 120	Arg	Phe	Ala	Lys	Leu	Leu	Ser
Asp	Arg	Lys	Lys	Leu	Arg	Ala 135	Asn	Lys	Ala	Ser	Tyr 140	Gly	Pro	Gly	Gln
Leu 145	Gly	Glu	Met	Val	Thr 150	Val	Leu	Ser	Ile	Asp 155	Gly	Gly	Gly	Ile	Arg 160
Gly	Ile	Ile	Pro	Ala 165	Thr	Ile	Leu	Glu	Phe 170	Leu	Glu	Gly	Gln	Leu	Gln 175
Glu	Met	Asp	Asn 180	Asn	Ala	Asp	Ala	Arg 185	Leu	Ala	Asp	Tyr	Phe	Asp	Val
Ile	Gly	Gly 195	Thr	Ser	Thr	Gly	Gly 200	Leu	Leu	Thr	Ala	Met 205	Ile	Ser	Thr
Pro	Asn 210	Glu	Asn	Asn	Arg	Pro	Phe 215	Ala	Ala	Ala	Lys	Glu	Ile	Val	Pro
Phe 225	Tyr	Phe	Glu	His	Gly 230	Pro	Gln	Ile	Phe	Asn 235	Pro	Ser	Gly	Gln	Ile 240
Leu	Gly	Pro	Lys	Tyr 245	Asp	Gly	Lys	Tyr	Leu	Met 250	Gln	Val	Leu	Gln	Glu 255
Lys	Leu	Gly	Glu 260	Thr	Arg	Val	His	Gln 265	Ala	Leu	Thr	Glu	Val	Val	Ile 270
Ser	Ser	Phe 275	Asp	Ile	Lys	Thr	Asn 280	Lys	Pro	Val	Ile	Phe	Thr	Lys	Ser
Asn 290	Leu	Ala	Asn	Ser	Pro	Glu 295	Leu	Asp	Ala	Lys	Met 300	Tyr	Asp	Ile	Ser
Tyr 305	Ser	Thr	Ala	Ala	Ala 310	Pro	Thr	Tyr	Phe	Pro 315	Pro	His	Tyr	Phe	Val 320
Thr	Asn	Thr	Ser	Asn 325	Gly	Asp	Glu	Tyr	Glu 330	Phe	Asn	Leu	Val	Asp	Gly 335
Ala	Val	Ala	Thr 340	Val	Ala	Asp	Pro	Ala 345	Leu	Leu	Ser	Ile	Ser	Val	Ala 350
Thr	Arg	Leu 355	Ala	Gln	Lys	Asp	Pro 360	Ala	Phe	Ala	Ser	Ile 365	Arg		

<210> 22

<211> 1128

<212> DNA

<213> synthetic

<220>

<221> DNA

<222> (1)..(1128)

<223> pMON37405 sequence encoding permutein protein

<400> 22

tcgagaaaag agaggctgaa gctaatacta gtaatggaga tgaatatgag ttcaatcttg	60
ttgatgggtgc tgttgctact gttgctgac cggcggttatt atccattagc gttgcaacga	120
gacttgcaca aaaggatcca gcatttgctt caattaggtc attgaattac aaaaaaatgc	180
tgttgctctc attaggcact ggcactactt cagagtttga taaaacatat acagcaaaaag	240
aggcagctac ctggactgct gtacattgga tgtagttat acagaaaatg actgatgcag	300
caagttctta catgactgat tattaccttt ctactgcttt tcaagctctt gattcaaaaa	360
acaattacct caggggtcaa gaaaatgcat taacaggcac aactactgaa atggatgatg	420
cttctgaggc taatatggaa ttattagtac aagttggtga aaacttattg aagaaaccag	480
tttccgaaga caatcctgaa acctatgagg aagctctaaa gaggtttgca aaattgctct	540
ctgataggaa gaaactccga gcaaacaag cttcttatgg accaggacag ttgggagaaa	600
tggtgactgt tcttagtatt gatggagggtg gaattagagg gatcattccg gctaccattc	660
tcgaatttct tgaaggacaa cttcaggaaa tggacaataa tgcagatgca agacttgcat	720
attactttga tgtaattgga ggaacaagta caggagggtt attgactgct atgataagta	780
ctccaaatga aaacaatcga ccttttgctg ctgccaaaga aattgtacct ttttacttcg	840
aacatggccc tcagattttt aatcctagtgt gtcaaatttt aggcccaaaa tatgatggaa	900
aatatcttat gcaagttctt caagaaaaac ttggagaaac tcgtgtgcat caagctttga	960
cagaagttgt catctcaagc ttgacatca aaacaaataa gccagtaata ttcactaagt	1020
caaatttagc aaactctcca gaattggatg ctaagatgta tgacataagt tattccacag	1080
cagcagctcc aacatatttt cctccgcatt actttgttac ttaatgag	1128

<210> 23

<211> 366

<212> PRT

<213> synthetic

<220>

<221> Protein

<222> (1)..(366)

<223> Permuterin protein encoded by pMON37405 sequence

<400> 23

Asn	Thr	Ser	Asn	Gly	Asp	Glu	Tyr	Glu	Phe	Asn	Leu	Val	Asp	Gly	Ala	
1				5					10					15		
Val	Ala	Thr	Val	Ala	Asp	Pro	Ala	Leu	Leu	Ser	Ile	Ser	Val	Ala	Thr	
			20					25					30			
Arg	Leu	Ala	Gln	Lys	Asp	Pro	Ala	Phe	Ala	Ser	Ile	Arg	Ser	Leu	Asn	
		35					40					45				
Tyr	Lys	Lys	Met	Leu	Leu	Leu	Ser	Leu	Gly	Thr	Gly	Thr	Thr	Ser	Glu	
	50					55					60					
Phe	Asp	Lys	Thr	Tyr	Thr	Ala	Lys	Glu	Ala	Ala	Thr	Trp	Thr	Ala	Val	
65					70					75					80	
His	Trp	Met	Leu	Val	Ile	Gln	Lys	Met	Thr	Asp	Ala	Ala	Ser	Ser	Tyr	
			85						90					95		
Met	Thr	Asp	Tyr	Tyr	Leu	Ser	Thr	Ala	Phe	Gln	Ala	Leu	Asp	Ser	Lys	
			100					105					110			
Asn	Asn	Tyr	Leu	Arg	Val	Gln	Glu	Asn	Ala	Leu	Thr	Gly	Thr	Thr	Thr	
		115					120					125				
Glu	Met	Asp	Asp	Ala	Ser	Glu	Ala	Asn	Met	Glu	Leu	Leu	Val	Gln	Val	
	130					135					140					
Gly	Glu	Asn	Leu	Leu	Lys	Lys	Pro	Val	Ser	Glu	Asp	Asn	Pro	Glu	Thr	
145					150					155					160	
Tyr	Glu	Glu	Ala	Leu	Lys	Arg	Phe	Ala	Lys	Leu	Leu	Ser	Asp	Arg	Lys	
			165						170					175		
Lys	Leu	Arg	Ala	Asn	Lys	Ala	Ser	Tyr	Gly	Pro	Gly	Gln	Leu	Gly	Glu	
			180					185					190			
Met	Val	Thr	Val	Leu	Ser	Ile	Asp	Gly	Gly	Gly	Ile	Arg	Gly	Ile	Ile	
		195					200					205				
Pro	Ala	Thr	Ile	Leu	Glu	Phe	Leu	Glu	Gly	Gln	Leu	Gln	Glu	Met	Asp	
	210					215						220				
Asn	Asn	Ala	Asp	Ala	Arg	Leu	Ala	Asp	Tyr	Phe	Asp	Val	Ile	Gly	Gly	
225					230					235					240	
Thr	Ser	Thr	Gly	Gly	Leu	Leu	Thr	Ala	Met	Ile	Ser	Thr	Pro	Asn	Glu	
			245						250					255		
Asn	Asn	Arg	Pro	Phe	Ala	Ala	Ala	Lys	Glu	Ile	Val	Pro	Phe	Tyr	Phe	
			260					265					270			
Glu	His	Gly	Pro	Gln	Ile	Phe	Asn	Pro	Ser	Gly	Gln	Ile	Leu	Gly	Pro	
		275					280					285				

Lys Tyr Asp Gly Lys Tyr Leu Met Gln Val Leu Gln Glu Lys Leu Gly  
 290 295 300  
 Glu Thr Arg Val His Gln Ala Leu Thr Glu Val Val Ile Ser Ser Phe  
 305 310 315 320  
 Asp Ile Lys Thr Asn Lys Pro Val Ile Phe Thr Lys Ser Asn Leu Ala  
 325 330 335  
 Asn Ser Pro Glu Leu Asp Ala Lys Met Tyr Asp Ile Ser Tyr Ser Thr  
 340 345 350  
 Ala Ala Ala Pro Thr Tyr Phe Pro Pro His Tyr Phe Val Thr  
 355 360 365

<210> 24

<211> 1128

<212> DNA

<213> synthetic

<220>

<221> DNA

<222> (1) .. (1128)

<223> pMON37406 sequence encoding permutein protein

<400> 24

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cgcattactt tgttactaat actagtaatg gagatgaata tgagttcaat cttgttgatg	120
gtgctgttgc tactgttgct gatccggcgt tattatccat tagcgttgca acgagacttg	180
cacaaaagga tccagcattt gcttcaatta ggtcattgaa ttacaaaaaa atgctgttgc	240
tctcattagg cactggcact acttcagagt ttgataaaac atatacagca aaagaggcag	300
ctacctggac tgctgtacat tggatgtag ttatacagaa aatgactgat gcagcaagtt	360
cttacatgac tgattattac ctttctactg cttttcaagc tcttgattca aaaaacaatt	420
acctcagggt tcaagaaaat gcattaacag gcacaactac tgaaatggat gatgcttctg	480
aggctaatat ggaattatta gtacaagttg gtgaaaactt attgaagaaa ccagtttccg	540
aagacaatcc tgaaacctat gaggaagctc taaagagggt tgcaaaattg ctctctgata	600
ggaagaaact ccgagcaaac aaagcttctt atggaccagg acagttggga gaaatggtga	660
ctgttcttag tattgatgga ggtggaatta gagggatcat tccggctacc attctcgaat	720
ttcttgaagg acaacttcag gaaatggaca ataatgcaga tgcaagactt gcagattact	780
ttgatgtaat tggaggaaca agtacaggag gtttattgac tgctatgata agtactccaa	840

atgaaaacaa tcgacccttt gctgctgcc aagaaattgt acctttttac ttcgaacatg 900  
gccctcagat ttttaatcct agtgggtcaaa ttttagggcc aaaatatgat ggaaaatatc 960  
ttatgcaagt tcttcaagaa aaacttggag aaactcgtgt gcatcaagct ttgacagaag 1020  
ttgtcatctc aagctttgac atcaaaacaa ataagccagt aatattcact aagtcaaatt 1080  
tagcaaactc tccagaattg gatgctaaga tgtatgacat ataatgag 1128

<210> 25

<211> 366

<212> PRT

<213> synthetic

<220>

<221> Protein

<222> (1)..(366)

<223> Permutin protein encoded by pMON37406

<400> 25

Ser	Tyr	Ser	Thr	Ala	Ala	Ala	Pro	Thr	Tyr	Phe	Pro	Pro	His	Tyr	Phe	1	5	10	15
Val	Thr	Asn	Thr	Ser	Asn	Gly	Asp	Glu	Tyr	Glu	Phe	Asn	Leu	Val	Asp	20	25	30	
Gly	Ala	Val	Ala	Thr	Val	Ala	Asp	Pro	Ala	Leu	Leu	Ser	Ile	Ser	Val	35	40	45	
Ala	Thr	Arg	Leu	Ala	Gln	Lys	Asp	Pro	Ala	Phe	Ala	Ser	Ile	Arg	Ser	50	55	60	
Leu	Asn	Tyr	Lys	Lys	Met	Leu	Leu	Leu	Ser	Leu	Gly	Thr	Gly	Thr	Thr	65	70	75	80
Ser	Glu	Phe	Asp	Lys	Thr	Tyr	Thr	Ala	Lys	Glu	Ala	Ala	Thr	Trp	Thr	85	90	95	
Ala	Val	His	Trp	Met	Leu	Val	Ile	Gln	Lys	Met	Thr	Asp	Ala	Ala	Ser	100	105	110	
Ser	Tyr	Met	Thr	Asp	Tyr	Tyr	Leu	Ser	Thr	Ala	Phe	Gln	Ala	Leu	Asp	115	120	125	
Ser	Lys	Asn	Asn	Tyr	Leu	Arg	Val	Gln	Glu	Asn	Ala	Leu	Thr	Gly	Thr	130	135	140	
Thr	Thr	Glu	Met	Asp	Asp	Ala	Ser	Glu	Ala	Asn	Met	Glu	Leu	Leu	Val	145	150	155	160

Gln Val Gly Glu Asn Leu Leu Lys Lys Pro Val Ser Glu Asp Asn Pro  
 165 170 175  
 Glu Thr Tyr Glu Glu Ala Leu Lys Arg Phe Ala Lys Leu Leu Ser Asp  
 180 185 190  
 Arg Lys Lys Leu Arg Ala Asn Lys Ala Ser Tyr Gly Pro Gly Gln Leu  
 195 200 205  
 Gly Glu Met Val Thr Val Leu Ser Ile Asp Gly Gly Gly Ile Arg Gly  
 210 215 220  
 Ile Ile Pro Ala Thr Ile Leu Glu Phe Leu Glu Gly Gln Leu Gln Glu  
 225 230 235 240  
 Met Asp Asn Asn Ala Asp Ala Arg Leu Ala Asp Tyr Phe Asp Val Ile  
 245 250 255  
 Gly Gly Thr Ser Thr Gly Gly Leu Leu Thr Ala Met Ile Ser Thr Pro  
 260 265 270  
 Asn Glu Asn Asn Arg Pro Phe Ala Ala Ala Lys Glu Ile Val Pro Phe  
 275 280 285  
 Tyr Phe Glu His Gly Pro Gln Ile Phe Asn Pro Ser Gly Gln Ile Leu  
 290 295 300  
 Gly Pro Lys Tyr Asp Gly Lys Tyr Leu Met Gln Val Leu Gln Glu Lys  
 305 310 315 320  
 Leu Gly Glu Thr Arg Val His Gln Ala Leu Thr Glu Val Val Ile Ser  
 325 330 335  
 Ser Phe Asp Ile Lys Thr Asn Lys Pro Val Ile Phe Thr Lys Ser Asn  
 340 345 350  
 Leu Ala Asn Ser Pro Glu Leu Asp Ala Lys Met Tyr Asp Ile  
 355 360 365

<210> 26

<211> 1128

<212> DNA

<213> synthetic

<220>

<221> DNA

<222> (1)..(1128)

<223> pMON37407 sequence encoding permutein protein

<400> 26

tcgagaaaag agaggctgaa gctacatata cagcaaaaga ggcagctacc tggactgctg 60

tacattggat gttagttata cagaaaatga ctgatgcagc aagttcttac atgactgatt 120

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attacctttc tactgctttt caagctcttg attcaaaaaa caattacctc aggggttcaag      180
aaaatgcatt aacaggcaca actactgaaa tggatgatgc ttctgaggct aatatggaat      240
tattagtaca agttggtgaa aacttattga agaaaccagt ttccgaagac aatcctgaaa      300
cctatgagga agctctaaag aggtttgcaa aattgctctc tgataggaag aaactccgat      360
caaacaaagc ttcttatgga ccaggacagt tgggagaaat ggtgactggt cttagtattg      420
atggaggtgg aattagaggg atcattccgg ctaccattct cgaatttctt gaaggacaac      480
ttcaggaaat ggacaataat gcagatgcaa gacttgcaga ttactttgat gtaattggag      540
gaacaagtac aggaggttta ttgactgcta tgataagtac tccaaatgaa aacaatcgac      600
cctttgctgc tgccaaagaa attgtacctt tttacttcga acatggccct cagattttta      660
atcctagtgg tcaaatttta ggcccaaaat atgatggaaa atatcttatg caagttcttc      720
aagaaaaact tggagaaact cgtgtgcatc aagctttgac agaagttgtc atctcaagct      780
ttgacatcaa aacaaataag ccagtaatat tactaagtc aaatttagca aactctccag      840
aattggatgc taagatgtat gacataagtt attccacagc agcagctcca acatattttc      900
ctccgcatta ctttgttact aatactagta atggagatga atatgagttc aatcttgttg      960
atggtgctgt tgctactggt gctgatccgg cgttattatc cattagcgtt gcaacgagac     1020
ttgcacaaaa ggatccagca tttgcttcaa ttaggtcatt gaattacaaa aaaatgctgt     1080
tgctctcatt aggcactggc actacttcag agtttgataa ataatgag                       1128

```

<210> 27

<211> 366

<212> PRT

<213> synthetic

<220>

<221> Protein

<222> (1)..(366)

<223> Permutein protein encoded by pMON37407 sequence

<400> 27

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Thr Tyr Thr Ala Lys Glu Ala Ala Thr Trp Thr Ala Val His Trp Met
1           5           10           15
Leu Val Ile Gln Lys Met Thr Asp Ala Ala Ser Ser Tyr Met Thr Asp
                20                25                30
Tyr Tyr Leu Ser Thr Ala Phe Gln Ala Leu Asp Ser Lys Asn Asn Tyr

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35							40				45				
Leu	Arg	Val	Gln	Glu	Asn	Ala	Leu	Thr	Gly	Thr	Thr	Thr	Glu	Met	Asp
50						55					60				
Asp	Ala	Ser	Glu	Ala	Asn	Met	Glu	Leu	Leu	Val	Gln	Val	Gly	Glu	Asn
65					70					75					80
Leu	Leu	Lys	Lys	Pro	Val	Ser	Glu	Asp	Asn	Pro	Glu	Thr	Tyr	Glu	Glu
				85					90					95	
Ala	Leu	Lys	Arg	Phe	Ala	Lys	Leu	Leu	Ser	Asp	Arg	Lys	Lys	Leu	Arg
			100					105					110		
Ser	Asn	Lys	Ala	Ser	Tyr	Gly	Pro	Gly	Gln	Leu	Gly	Glu	Met	Val	Thr
		115					120					125			
Val	Leu	Ser	Ile	Asp	Gly	Gly	Gly	Ile	Arg	Gly	Ile	Ile	Pro	Ala	Thr
	130					135						140			
Ile	Leu	Glu	Phe	Leu	Glu	Gly	Gln	Leu	Gln	Glu	Met	Asp	Asn	Asn	Ala
145					150					155					160
Asp	Ala	Arg	Leu	Ala	Asp	Tyr	Phe	Asp	Val	Ile	Gly	Gly	Thr	Ser	Thr
				165					170					175	
Gly	Gly	Leu	Leu	Thr	Ala	Met	Ile	Ser	Thr	Pro	Asn	Glu	Asn	Asn	Arg
			180					185					190		
Pro	Phe	Ala	Ala	Ala	Lys	Glu	Ile	Val	Pro	Phe	Tyr	Phe	Glu	His	Gly
		195					200					205			
Pro	Gln	Ile	Phe	Asn	Pro	Ser	Gly	Gln	Ile	Leu	Gly	Pro	Lys	Tyr	Asp
	210					215					220				
Gly	Lys	Tyr	Leu	Met	Gln	Val	Leu	Gln	Glu	Lys	Leu	Gly	Glu	Thr	Arg
225					230					235					240
Val	His	Gln	Ala	Leu	Thr	Glu	Val	Val	Ile	Ser	Ser	Phe	Asp	Ile	Lys
				245					250					255	
Thr	Asn	Lys	Pro	Val	Ile	Phe	Thr	Lys	Ser	Asn	Leu	Ala	Asn	Ser	Pro
			260					265					270		
Glu	Leu	Asp	Ala	Lys	Met	Tyr	Asp	Ile	Ser	Tyr	Ser	Thr	Ala	Ala	Ala
		275					280					285			
Pro	Thr	Tyr	Phe	Pro	Pro	His	Tyr	Phe	Val	Thr	Asn	Thr	Ser	Asn	Gly
	290					295					300				
Asp	Glu	Tyr	Glu	Phe	Asn	Leu	Val	Asp	Gly	Ala	Val	Ala	Thr	Val	Ala
305					310					315					320
Asp	Pro	Ala	Leu	Leu	Ser	Ile	Ser	Val	Ala	Thr	Arg	Leu	Ala	Gln	Lys
				325					330					335	
Asp	Pro	Ala	Phe	Ala	Ser	Ile	Arg	Ser	Leu	Asn	Tyr	Lys	Lys	Met	Leu
			340					345					350		
Leu	Leu	Ser	Leu	Gly	Thr	Gly	Thr	Thr	Ser	Glu	Phe	Asp	Lys		
		355				360						365			

<210> 28

<211> 1128



<212> DNA

<213> synthetic

<220>

<221> DNA

<222> (1)..(1128)

<223> pMON37408 sequence encoding permutein protein

<400> 28  
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cttctgaggc taatatggaa ttattagtagc aagttggtga aaacttattg aagaaaccag 120  
tttccgaaga caatcctgaa acctatgagg aagctctaaa gaggtttgca aaattgctct 180  
ctgataggaa gaaactccga gcaaacaaag cttcttatgg accaggacag ttgggagaaa 240  
tggtgactgt tcttagtatt gatggagggtg gaattagagg gatcattccg gctaccattc 300  
tcgaatttct tgaaggacaa cttcaggaaa tggacaataa tgcagatgca agacttgacg 360  
attactttga tgtaattgga ggaacaagta caggagggttt attgactgct atgataagta 420  
ctccaaatga aaacaatcga ccctttgctg ctgccaaaga aattgtacct ttttacttcg 480  
aacatggccc tcagatTTTT aatcctagtg gtcaaatttt aggcccaaaa tatgatggaa 540  
aatatcttat gcaagttctt caagaaaaac ttggagaaac tcgtgtgcat caagctttga 600  
cagaagttgt catctcaagc ttgacatca aaacaaataa gccagtaata ttcactaagt 660  
caaatttagc aaactctcca gaattggatg ctaagatgta tgacataagt tattccacag 720  
cagcagctcc aacatatttt cctccgcatt actttgttac taatactagt aatggagatg 780  
aatatgagtt caatcttggt gatggtgctg ttgctactgt tgctgatccg gcgttattat 840  
ccattagcgt tgcaacgaga cttgcacaaa aggatccagc atttgcttca attaggtcat 900  
tgaattacaa aaaaatgctg ttgctctcat taggcactgg cactacttca gagtttgata 960  
aaacatatac agcaaaagag gcagctacct ggactgctgt acattggatg ttagttatac 1020  
agaaaatgac tgatgcagca agttcttaca tgactgatta ttacctttct actgcttttc 1080  
aagctcttga ttcaaaaaac aattacctca gggttcaaga ataatgag 1128

<210> 29

<211> 366

<212> PRT

<213> synthetic

<220>

<221> Protein

<222> (1) . . (366)

<223> Permuterin protein encoded by pMON37408

<400> 29

Asn 1	Ala	Leu	Thr	Gly 5	Thr	Thr	Thr	Glu 10	Met	Asp	Asp	Ala	Ser	Glu 15	Ala
Asn	Met	Glu	Leu 20	Leu	Val	Gln	Val	Gly 25	Glu	Asn	Leu	Leu	Lys 30	Lys	Pro
Val	Ser	Glu 35	Asp	Asn	Pro	Glu	Thr 40	Tyr	Glu	Glu	Ala	Leu 45	Lys	Arg	Phe
Ala	Lys 50	Leu	Leu	Ser	Asp	Arg 55	Lys	Lys	Leu	Arg	Ala 60	Asn	Lys	Ala	Ser
Tyr 65	Gly	Pro	Gly	Gln	Leu 70	Gly	Glu	Met	Val	Thr 75	Val	Leu	Ser	Ile	Asp 80
Gly	Gly	Gly	Ile	Arg 85	Gly	Ile	Ile	Pro	Ala 90	Thr	Ile	Leu	Glu	Phe 95	Leu
Glu	Gly	Gln	Leu 100	Gln	Glu	Met	Asp	Asn 105	Asn	Ala	Asp	Ala	Arg 110	Leu	Ala
Asp	Tyr	Phe 115	Asp	Val	Ile	Gly	Gly 120	Thr	Ser	Thr	Gly	Gly 125	Leu	Leu	Thr
Ala	Met 130	Ile	Ser	Thr	Pro	Asn 135	Glu	Asn	Asn	Arg	Pro 140	Phe	Ala	Ala	Ala
Lys 145	Glu	Ile	Val	Pro	Phe 150	Tyr	Phe	Glu	His	Gly 155	Pro	Gln	Ile	Phe	Asn 160
Pro	Ser	Gly	Gln	Ile 165	Leu	Gly	Pro	Lys	Tyr 170	Asp	Gly	Lys	Tyr	Leu	Met 175
Gln	Val	Leu	Gln 180	Glu	Lys	Leu	Gly	Glu 185	Thr	Arg	Val	His	Gln 190	Ala	Leu
Thr	Glu	Val 195	Val	Ile	Ser	Ser	Phe 200	Asp	Ile	Lys	Thr	Asn 205	Lys	Pro	Val
Ile	Phe 210	Thr	Lys	Ser	Asn	Leu 215	Ala	Asn	Ser	Pro	Glu 220	Leu	Asp	Ala	Lys
Met 225	Tyr	Asp	Ile	Ser	Tyr 230	Ser	Thr	Ala	Ala	Ala 235	Pro	Thr	Tyr	Phe	Pro 240
Pro	His	Tyr	Phe	Val 245	Thr	Asn	Thr	Ser	Asn 250	Gly	Asp	Glu	Tyr	Glu 255	Phe
Asn	Leu	Val	Asp 260	Gly	Ala	Val	Ala	Thr 265	Val	Ala	Asp	Pro	Ala 270	Leu	Leu

Ser Ile Ser Val Ala Thr Arg Leu Ala Gln Lys Asp Pro Ala Phe Ala  
 275 280 285  
 Ser Ile Arg Ser Leu Asn Tyr Lys Lys Met Leu Leu Leu Ser Leu Gly  
 290 295 300  
 Thr Gly Thr Thr Ser Glu Phe Asp Lys Thr Tyr Thr Ala Lys Glu Ala  
 305 310 315 320  
 Ala Thr Trp Thr Ala Val His Trp Met Leu Val Ile Gln Lys Met Thr  
 325 330 335  
 Asp Ala Ala Ser Ser Tyr Met Thr Asp Tyr Tyr Leu Ser Thr Ala Phe  
 340 345 350  
 Gln Ala Leu Asp Ser Lys Asn Asn Tyr Leu Arg Val Gln Glu  
 355 360 365

<210> 30

<211> 1158

<212> DNA

<213> synthetic

<220>

<221> DNA

<222> (1)..(1158)

<223> pMON40701 sequence encoding permutein protein

<400> 30  
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 accttcgccc agctcggcga gatggtgacc gtgctctcca tcgacggcgg tggcatcagg 120  
 ggcacatccc cgccaccat cctggagttc ctggagggcc aactccagga gatggacaac 180  
 aacgccgacg cccgcctggc cgactacttc gacgtgatcg gtggcaccag caccggcggt 240  
 ctctgaccg ccatgatctc cactccgaac gagaacaacc gcccttcgc cgctgcgaag 300  
 gagatcgctc cgttctactt cgaacacggc cctcagattt tcaaccctc ggggtcaaata 360  
 ctggggccca agtacgacg caagtacctt atgcaagtgc ttcaggagaa gctgggagcag 420  
 actaggggtgc accaggcgct gaccgaggtc gtcactctcca gcttcgacat caagaccaac 480  
 aagccagtca tcttcaccaa gtccaacctg gccaacagcc cggagctgga cgctaagatg 540  
 tacgacatct cctactccac tgctgcccgt cccacgtact tccctccgca ctacttcgtc 600  
 accaacacca gcaacggcga cgagtacgag ttcaaccttg ttgacgggtgc ggtggctacg 660  
 gtggcggaacc cggcgctcct gtccatcagc gtcgcccacgc gcctggccca gaaggatcca 720

gccttcgcta gcattaggag cctcaactac aagaagatgc tgctgctcag cctggggcact 780  
ggcacgacct ccgagttcga caagacctac actgcccaagg aggccgctac ctggaccgcc 840  
gtccattgga tgctgggtcat ccagaagatg acggacgccg cttccagcta catgaccgac 900  
tactacctct ccactgcgtt ccaggcgctt gactccaaga acaactacct ccgtgttcag 960  
gagaatgccc tcactggcac cacgaccgag atggacgatg cctccgaggc caacatggag 1020  
ctgctcgtcc aggtgggtga gaacctcctg aagaagcccg tctccgaaga caatcccag 1080  
acctatgagg aagcgctcaa gcgctttgcc aagctgctct ctgataggaa gaaactccgc 1140  
gctaacaagg ccagctac 1158

<210> 31

<211> 386

<212> PRT

<213> synthetic

<220>

<221> Protein

<222> (1)..(386)

<223> Permutin protein encoded by pMON40701 sequence

<400> 31

Met Ala Thr Thr Lys Ser Phe Leu Ile Leu Ile Phe Met Ile Leu Ala  
1 5 10 15  
Thr Thr Ser Ser Thr Phe Ala Gln Leu Gly Glu Met Val Thr Val Leu  
20 25 30  
Ser Ile Asp Gly Gly Gly Ile Arg Gly Ile Ile Pro Ala Thr Ile Leu  
35 40 45  
Glu Phe Leu Glu Gly Gln Leu Gln Glu Met Asp Asn Asn Ala Asp Ala  
50 55 60  
Arg Leu Ala Asp Tyr Phe Asp Val Ile Gly Gly Thr Ser Thr Gly Gly  
65 70 75 80  
Leu Leu Thr Ala Met Ile Ser Thr Pro Asn Glu Asn Asn Arg Pro Phe  
85 90 95  
Ala Ala Ala Lys Glu Ile Val Pro Phe Tyr Phe Glu His Gly Pro Gln  
100 105 110  
Ile Phe Asn Pro Ser Gly Gln Ile Leu Gly Pro Lys Tyr Asp Gly Lys  
115 120 125  
Tyr Leu Met Gln Val Leu Gln Glu Lys Leu Gly Glu Thr Arg Val His

130

135

140

Gln Ala Leu Thr Glu Val Val Ile Ser Ser Phe Asp Ile Lys Thr Asn  
 145 150 155 160  
 Lys Pro Val Ile Phe Thr Lys Ser Asn Leu Ala Asn Ser Pro Glu Leu  
 165 170 175  
 Asp Ala Lys Met Tyr Asp Ile Ser Tyr Ser Thr Ala Ala Ala Pro Thr  
 180 185 190  
 Tyr Phe Pro Pro His Tyr Phe Val Thr Asn Thr Ser Asn Gly Asp Glu  
 195 200 205  
 Tyr Glu Phe Asn Leu Val Asp Gly Ala Val Ala Thr Val Ala Asp Pro  
 210 215 220  
 Ala Leu Leu Ser Ile Ser Val Ala Thr Arg Leu Ala Gln Lys Asp Pro  
 225 230 235 240  
 Ala Phe Ala Ser Ile Arg Ser Leu Asn Tyr Lys Lys Met Leu Leu Leu  
 245 250 255  
 Ser Leu Gly Thr Gly Thr Thr Ser Glu Phe Asp Lys Thr Tyr Thr Ala  
 260 265 270  
 Lys Glu Ala Ala Thr Trp Thr Ala Val His Trp Met Leu Val Ile Gln  
 275 280 285  
 Lys Met Thr Asp Ala Ala Ser Ser Tyr Met Thr Asp Tyr Tyr Leu Ser  
 290 295 300  
 Thr Ala Phe Gln Ala Leu Asp Ser Lys Asn Asn Tyr Leu Arg Val Gln  
 305 310 315 320  
 Glu Asn Ala Leu Thr Gly Thr Thr Thr Glu Met Asp Asp Ala Ser Glu  
 325 330 335  
 Ala Asn Met Glu Leu Leu Val Gln Val Gly Glu Asn Leu Leu Lys Lys  
 340 345 350  
 Pro Val Ser Glu Asp Asn Pro Glu Thr Tyr Glu Glu Ala Leu Lys Arg  
 355 360 365  
 Phe Ala Lys Leu Leu Ser Asp Arg Lys Lys Leu Arg Ala Asn Lys Ala  
 370 375 380

Ser Tyr  
385

&lt;210&gt; 32

&lt;211&gt; 1167

&lt;212&gt; DNA

&lt;213&gt; synthetic

&lt;220&gt;

&lt;221&gt; DNA

&lt;222&gt; (1)..(1167)

<223> pMON40703 sequence encoding permutein protein

<400> 32

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accttcgccca gcctcaacta caagaagatg ctgctgctca gcctgggcac tggcacgacc	120
tccgagttcg acaagacctt cactgccaaag gaggccgcta cctggaccgc cgtccattgg	180
atgctggtca tccagaagat gacggacgcc gcttccagct acatgaccga ctactacctc	240
tccactgcgt tccaggcgct tgactccaag aacaactacc tccgtgttca ggagaatgcc	300
ctcactggca ccacgaccga gatggacgat gcctccgagg ccaacatgga gctgctcgtc	360
caggtgggtg agaacctcct gaagaagccc gtctccgaag acaatcccga gacctatgag	420
gaagcgctca agcgctttgc caagctgctc tctgatagga agaaactccg cgctaacaag	480
gccagctacg gaccaggaca gctcggcgag atggtgaccg tgctctccat cgacggcggt	540
ggcatcaggg gcatcatccc ggccaccatc ctggagttcc tggagggcca actccaggag	600
atggacaaca acgccgacgc ccgcctggcc gactacttcg acgtgatcgg tggcaccagc	660
accggcggtc tcctgaccgc catgatctcc actccgaacg agaacaaccg ccccttcgcc	720
gctgcgaagg agatcgctcc gttctacttc gaacacggcc ctcagatttt caaccctcg	780
ggtcaaattc tgggcccaca gtacgacggc aagtacctta tgcaagtgtc tcaggagaag	840
ctgggcgaga ctagggtgca ccaggcgctg accgaggtcg tcatctccag cttcgacatc	900
aagaccaaca agccagtcac cttcaccaag tccaacctgg ccaacagccc ggagctggac	960
gctaagatgt acgacatctc ctactccact gctgccgctc ccacgtactt ccctccgcac	1020
tacttcgtca ccaacaccag caacggcgac gagtacgagt tcaaccttgt tgacgggtgcg	1080
gtggctacgg tggcggaacc ggcgctcctg tccatcagcg tcgccacgcg cctggcccag	1140
aaggatccag ccttcgctag cattagg	1167

<210> 33

<211> 389

<212> PRT

<213> synthetic

<220>

<221> Protein

<222> (1) .. (389)

<223> Permutein protein encoded by pMON40703 sequence

<400> 33

Met Ala Thr Thr Lys Ser Phe Leu Ile Leu Ile Phe Met Ile Leu Ala  
1 5 10 15  
Thr Thr Ser Ser Thr Phe Ala Ser Leu Asn Tyr Lys Lys Met Leu Leu  
20 25 30  
Leu Ser Leu Gly Thr Gly Thr Thr Ser Glu Phe Asp Lys Thr Tyr Thr  
35 40 45  
Ala Lys Glu Ala Ala Thr Trp Thr Ala Val His Trp Met Leu Val Ile  
50 55 60  
Gln Lys Met Thr Asp Ala Ala Ser Ser Tyr Met Thr Asp Tyr Tyr Leu  
65 70 75 80  
Ser Thr Ala Phe Gln Ala Leu Asp Ser Lys Asn Asn Tyr Leu Arg Val  
85 90 95  
Gln Glu Asn Ala Leu Thr Gly Thr Thr Thr Glu Met Asp Asp Ala Ser  
100 105 110  
Glu Ala Asn Met Glu Leu Leu Val Gln Val Gly Glu Asn Leu Leu Lys  
115 120 125  
Lys Pro Val Ser Glu Asp Asn Pro Glu Thr Tyr Glu Glu Ala Leu Lys  
130 135 140  
Arg Phe Ala Lys Leu Leu Ser Asp Arg Lys Lys Leu Arg Ala Asn Lys  
145 150 155 160  
Ala Ser Tyr Gly Pro Gly Gln Leu Gly Glu Met Val Thr Val Leu Ser  
165 170 175  
Ile Asp Gly Gly Gly Ile Arg Gly Ile Ile Pro Ala Thr Ile Leu Glu  
180 185 190  
Phe Leu Glu Gly Gln Leu Gln Glu Met Asp Asn Asn Ala Asp Ala Arg  
195 200 205  
Leu Ala Asp Tyr Phe Asp Val Ile Gly Gly Thr Ser Thr Gly Gly Leu  
210 215 220  
Leu Thr Ala Met Ile Ser Thr Pro Asn Glu Asn Asn Arg Pro Phe Ala  
225 230 235 240  
Ala Ala Lys Glu Ile Val Pro Phe Tyr Phe Glu His Gly Pro Gln Ile  
245 250 255  
Phe Asn Pro Ser Gly Gln Ile Leu Gly Pro Lys Tyr Asp Gly Lys Tyr  
260 265 270  
Leu Met Gln Val Leu Gln Glu Lys Leu Gly Glu Thr Arg Val His Gln  
275 280 285  
Ala Leu Thr Glu Val Val Ile Ser Ser Phe Asp Ile Lys Thr Asn Lys  
290 295 300  
Pro Val Ile Phe Thr Lys Ser Asn Leu Ala Asn Ser Pro Glu Leu Asp  
305 310 315 320

Ala Lys Met Tyr Asp Ile Ser Tyr Ser Thr Ala Ala Ala Pro Thr Tyr  
325 330 335  
Phe Pro Pro His Tyr Phe Val Thr Asn Thr Ser Asn Gly Asp Glu Tyr  
340 345 350  
Glu Phe Asn Leu Val Asp Gly Ala Val Ala Thr Val Ala Asp Pro Ala  
355 360 365  
Leu Leu Ser Ile Ser Val Ala Thr Arg Leu Ala Gln Lys Asp Pro Ala  
370 375 380  
Phe Ala Ser Ile Arg  
385

<210> 34  
<211> 1167  
<212> DNA  
<213> synthetic

<220>  
<221> DNA  
<222> (1) .. (1167)  
<223> pMON40705 sequence encoding permutein protein

<400> 34  
atggccacca ccaagagctt cctcatcctg atcttcatga tcctggccac caccagcagc 60  
accttcgccca cctacactgc caaggaggcc gctacctgga ccgccgtcca ttggatgctg 120  
gtcatccaga agatgacgga cgccgcttcc agctacatga ccgactacta cctctccact 180  
gcgttccagg cgcttgactc caagaacaac tacctccgtg ttcaggagaa tgccctcact 240  
ggcaccacga ccgagatgga cgatgcctcc gaggccaaca tggagctgct cgtccaggtg 300  
ggtgagaacc tcctgaagaa gcccgctctcc gaagacaatc ccgagaccta tgaggaagcg 360  
ctcaagcgct ttgccaagct gctctctgat aggaagaaac tccgcgctaa caaggccagc 420  
tacggaccag gacagctcgg cgagatggtg accgtgctct ccacgcagcg cgggtggcatc 480  
aggggcatca tcccggccac catcctggag ttcttggagg gccaaactcca ggagatggac 540  
aacaacgccg acgcccgcct ggccgactac ttcgacgtga tcggtggcac cagcaccggc 600  
ggtctcctga ccgccatgat ctccactccg aacgagaaca accgcccctt cgccgctgcg 660  
aaggagatcg tcccgttcta cttcgaacac ggccctcaga ttttcaaccc ctcgggtcaa 720  
atcctggggc ccaagtacga cggcaagtac cttatgcaag tgcttcagga gaagctgggc 780  
gagactaggg tgcaccaggc gctgaccgag gtcgtcatct ccagcttcga catcaagacc 840



aacaagccag tcattcttcac caagtccaac ctggccaaca gcccgagct ggacgctaag 900  
atgtacgaca tctcctactc cactgctgcc gctcccacgt acttccctcc gcactacttc 960  
gtcaccaaca ccagcaacgg cgacgagtag gagttcaacc ttgttgacgg tgcggtggct 1020  
acgggtggcgg acccggcgct cctgtccatc agcgtcgcca cgcgcctggc ccagaaggat 1080  
ccagccttcg ctagcattag gagcctcaac tacaagaaga tgctgctgct cagcctgggc 1140  
actggcacga cctccgagtt cgacaag 1167

<210> 35

<211> 389

<212> PRT

<213> synthetic

<220>

<221> Protein

<222> (1)..(389)

<223> Permuted protein encoded by pMON40705

<400> 35

Met	Ala	Thr	Thr	Lys	Ser	Phe	Leu	Ile	Leu	Ile	Phe	Met	Ile	Leu	Ala	1	5	10	15
Thr	Thr	Ser	Ser	Thr	Phe	Ala	Thr	Tyr	Thr	Ala	Lys	Glu	Ala	Ala	Thr	20	25	30	
Trp	Thr	Ala	Val	His	Trp	Met	Leu	Val	Ile	Gln	Lys	Met	Thr	Asp	Ala	35	40	45	
Ala	Ser	Ser	Tyr	Met	Thr	Asp	Tyr	Tyr	Leu	Ser	Thr	Ala	Phe	Gln	Ala	50	55	60	
Leu	Asp	Ser	Lys	Asn	Asn	Tyr	Leu	Arg	Val	Gln	Glu	Asn	Ala	Leu	Thr	65	70	75	80
Gly	Thr	Thr	Thr	Glu	Met	Asp	Asp	Ala	Ser	Glu	Ala	Asn	Met	Glu	Leu	85	90	95	
Leu	Val	Gln	Val	Gly	Glu	Asn	Leu	Leu	Lys	Lys	Pro	Val	Ser	Glu	Asp	100	105	110	
Asn	Pro	Glu	Thr	Tyr	Glu	Glu	Ala	Leu	Lys	Arg	Phe	Ala	Lys	Leu	Leu	115	120	125	
Ser	Asp	Arg	Lys	Lys	Leu	Arg	Ala	Asn	Lys	Ala	Ser	Tyr	Gly	Pro	Gly	130	135	140	
Gln	Leu	Gly	Glu	Met	Val	Thr	Val	Leu	Ser	Ile	Asp	Gly	Gly	Gly	Ile	145	150	155	160

Arg Gly Ile Ile Pro Ala Thr Ile Leu Glu Phe Leu Glu Gly Gln Leu  
 165 170 175  
 Gln Glu Met Asp Asn Asn Ala Asp Ala Arg Leu Ala Asp Tyr Phe Asp  
 180 185 190  
 Val Ile Gly Gly Thr Ser Thr Gly Gly Leu Leu Thr Ala Met Ile Ser  
 195 200 205  
 Thr Pro Asn Glu Asn Asn Arg Pro Phe Ala Ala Ala Lys Glu Ile Val  
 210 215 220  
 Pro Phe Tyr Phe Glu His Gly Pro Gln Ile Phe Asn Pro Ser Gly Gln  
 225 230 235 240  
 Ile Leu Gly Pro Lys Tyr Asp Gly Lys Tyr Leu Met Gln Val Leu Gln  
 245 250 255  
 Glu Lys Leu Gly Glu Thr Arg Val His Gln Ala Leu Thr Glu Val Val  
 260 265 270  
 Ile Ser Ser Phe Asp Ile Lys Thr Asn Lys Pro Val Ile Phe Thr Lys  
 275 280 285  
 Ser Asn Leu Ala Asn Ser Pro Glu Leu Asp Ala Lys Met Tyr Asp Ile  
 290 295 300  
 Ser Tyr Ser Thr Ala Ala Ala Pro Thr Tyr Phe Pro Pro His Tyr Phe  
 305 310 315 320  
 Val Thr Asn Thr Ser Asn Gly Asp Glu Tyr Glu Phe Asn Leu Val Asp  
 325 330 335  
 Gly Ala Val Ala Thr Val Ala Asp Pro Ala Leu Leu Ser Ile Ser Val  
 340 345 350  
 Ala Thr Arg Leu Ala Gln Lys Asp Pro Ala Phe Ala Ser Ile Arg Ser  
 355 360 365  
 Leu Asn Tyr Lys Lys Met Leu Leu Leu Ser Leu Gly Thr Gly Thr Thr  
 370 375 380

Ser Glu Phe Asp Lys  
385

<210> 36

<211> 10

<212> PRT

<213> synthetic

<220>

<221> Protein

<222> (1)..(10)

<223> corn homolog peptide

<400> 36

Cys Ile Phe Asp Ser Thr Tyr Thr Ala Lys  
1 5 10

<210> 37

<211> 1161

<212> DNA

<213> Solanum cardiophyllum

<220>

<221> exon

<222> (1)..(1161)

<223> patatin homolog Pat17 nucleic acid and amino acid translation

<400> 37

atg gca act act aaa tct ttt tta att tta ata ttt atg ata tta gca 48  
Met Ala Thr Thr Lys Ser Phe Leu Ile Leu Ile Phe Met Ile Leu Ala  
1 5 10 15

act act agt tca aca ttt gct cag ttg gga gaa atg gtg act gtt ctt 96  
Thr Thr Ser Ser Thr Phe Ala Gln Leu Gly Glu Met Val Thr Val Leu  
20 25 30

agt att gat gga ggt gga att aga ggg atc att ccg gct acc att ctc 144  
Ser Ile Asp Gly Gly Gly Ile Arg Gly Ile Ile Pro Ala Thr Ile Leu  
35 40 45

gaa ttt ctt gaa gga caa ctt cag gaa atg gac aat aat gca gat gca 192  
Glu Phe Leu Glu Gly Gln Leu Gln Glu Met Asp Asn Asn Ala Asp Ala  
50 55 60

aga ctt gca gat tac ttt gat gta att gga gga aca agt aca gga ggt 240  
Arg Leu Ala Asp Tyr Phe Asp Val Ile Gly Gly Thr Ser Thr Gly Gly  
65 70 75 80

tta ttg act gct atg ata agt act cca aat gaa aac aat cga ccc ttt 288  
Leu Leu Thr Ala Met Ile Ser Thr Pro Asn Glu Asn Asn Arg Pro Phe  
85 90 95

gct gct gcc aaa gaa att gta cct ttt tac ttc gaa cat ggc cct cag 336  
Ala Ala Ala Lys Glu Ile Val Pro Phe Tyr Phe Glu His Gly Pro Gln  
100 105 110

att ttt aat cct agt ggt caa att tta ggc cca aaa tat gat gga aaa 384  
Ile Phe Asn Pro Ser Gly Gln Ile Leu Gly Pro Lys Tyr Asp Gly Lys  
115 120 125

tat ctt atg caa gtt ctt caa gaa aaa ctt gga gaa act cgt gtg cat 432  
Tyr Leu Met Gln Val Leu Gln Glu Lys Leu Gly Glu Thr Arg Val His  
130 135 140

caa gct ttg aca gaa gtt gtc atc tca agc ttt gac atc aaa aca aat Gln Ala Leu Thr Glu Val Val Ile Ser Ser Phe Asp Ile Lys Thr Asn 145 150 155 160	480
aag cca gta ata ttc act aag tca aat tta gca aac tct cca gaa ttg Lys Pro Val Ile Phe Thr Lys Ser Asn Leu Ala Asn Ser Pro Glu Leu 165 170 175	528
gat gct aag atg tat gac ata agt tat tcc aca gca gca gct cca aca Asp Ala Lys Met Tyr Asp Ile Ser Tyr Ser Thr Ala Ala Pro Thr 180 185 190	576
tat ttt cct ccg cat tac ttt gtt act aat act agt aat gga gat gaa Tyr Phe Pro Pro His Tyr Phe Val Thr Asn Thr Ser Asn Gly Asp Glu 195 200 205	624
tat gag ttc aat ctt gtt gat ggt gct gtt gct act gtt gct gat ccg Tyr Glu Phe Asn Leu Val Asp Gly Ala Val Ala Thr Val Ala Asp Pro 210 215 220	672
gcg tta tta tcc att agc gtt gca acg aga ctt gca caa aag gat cca Ala Leu Leu Ser Ile Ser Val Ala Thr Arg Leu Ala Gln Lys Asp Pro 225 230 235 240	720
gca ttt gct tca att agg tca ttg aat tac aaa aaa atg ctg ttg ctc Ala Phe Ala Ser Ile Arg Ser Leu Asn Tyr Lys Lys Met Leu Leu Leu 245 250 255	768
tca tta ggc act ggc act act tca gag ttt gat aaa aca tat aca gca Ser Leu Gly Thr Gly Thr Thr Ser Glu Phe Asp Lys Thr Tyr Thr Ala 260 265 270	816
aaa gag gca gct acc tgg act gct gta cat tgg atg tta gtt ata cag Lys Glu Ala Ala Thr Trp Thr Ala Val His Trp Met Leu Val Ile Gln 275 280 285	864
aaa atg act gat gca gca agt tct tac atg act gat tat tac ctt tct Lys Met Thr Asp Ala Ala Ser Ser Tyr Met Thr Asp Tyr Tyr Leu Ser 290 295 300	912
act gct ttt caa gct ctt gat tca aaa aac aat tac ctc agg gtt caa Thr Ala Phe Gln Ala Leu Asp Ser Lys Asn Asn Tyr Leu Arg Val Gln 305 310 315 320	960
gaa aat gca tta aca ggc aca act act gaa atg gat gat gct tct gag Glu Asn Ala Leu Thr Gly Thr Thr Thr Glu Met Asp Asp Ala Ser Glu 325 330 335	1008
gct aat atg gaa tta tta gta caa gtt ggt gaa aac tta ttg aag aaa Ala Asn Met Glu Leu Leu Val Gln Val Gly Glu Asn Leu Leu Lys Lys 340 345 350	1056
cca gtt tcc gaa gac aat cct gaa acc tat gag gaa gct cta aag agg Pro Val Ser Glu Asp Asn Pro Glu Thr Tyr Glu Glu Ala Leu Lys Arg 355 360 365	1104
ttt gca aaa ttg ctc tct gat agg aag aaa ctc cga gca aac aaa gct Phe Ala Lys Leu Leu Ser Asp Arg Lys Lys Leu Arg Ala Asn Lys Ala 370 375 380	1152
tct tat taa Ser Tyr 385	1161

<210> 38

<211> 1158

<212> DNA

<213> Solanum tuberosum

<220>

<221> DNA

<222> (1)..(1158)

<223> DNA sequence encoding a patatin (acyl lipid hydrolase) protein

<400> 38

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atggcaacta ctaaactctt tttaatttta atatttatga tattagcaac tactagttca      60
acatttgctc agttgggaga aatgggtgact gttcttagta ttgatggagg tggaattaga      120
gggatcattc cggctaccat tctcgaattt cttgaaggac aacttcagga aatggacaat      180
aatgcagatg caagacttgc agattacttt gatgtaattg gaggaacaag tacaggaggt      240
ttattgactg ctatgataag tactccaaat gaaaacaatc gaccctttgc tgctgccaaa      300
gaaattgtac ctttttactt cgaacatggc cctcagattt ttaatcctag tgggtcaaatt      360
ttaggcccaa aatatgatgg aaaatatctt atgcaagttc ttcaagaaaa acttggagaa      420
actcgtgtgc atcaagcttt gacagaagtt gtcattctca gctttgacat caaaacaaat      480
aagccagtaa tattcactaa gtcaaattta gcaaactctc cagaattgga tgctaagatg      540
tatgacataa gttattccac agcagcagct ccaacatatt ttctccgca ttactttggt      600
actaatacta gtaatggaga tgaatatgag ttcaatcttg ttgatgggtg tggttgctact      660
gttgctgata cggcggttatt atccattagc gttgcaacga gacttgcaca aaaggatcca      720
gcatttgctt caattagggtc attgaattac aaaaaaatgc tgttgctctc attaggcact      780
ggcactactt cagagtttga taaaacatat acagcaaaag aggcagctac ctggactgct      840
gtacattgga tgttagtatt acagaaaatg actgatgcag caagttctta catgactgat      900
tattaccttt ctactgcttt tcaagctctt gattcaaaaa acaattacct caggggttcaa      960
gaaaatgcat taacaggcac aactactgaa atggatgatg cttctgaggc taatatggaa     1020
ttattagtac aagttggtga aaacttattg aagaaaccag tttccgaaga caatcctgaa     1080
acctatgagg aagctctaaa gaggtttgca aaattgctct ctgataggaa gaaactccga     1140
gcaaacaaag cttcttat                                     1158
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<210> 39

<211> 386

<212> PRT

<213> potato

<220>

<221> Protein

<222> (1)..(386)

<223> potato patatin protein sequence

<400> 39

Met Ala Thr Thr Lys Ser Phe Leu Ile Leu Ile Phe Met Ile Leu Ala  
1 5 10 15  
Thr Thr Ser Ser Thr Phe Ala Gln Leu Gly Glu Met Val Thr Val Leu  
20 25 30  
Ser Ile Asp Gly Gly Gly Ile Arg Gly Ile Ile Pro Ala Thr Ile Leu  
35 40 45  
Glu Phe Leu Glu Gly Gln Leu Gln Glu Met Asp Asn Asn Ala Asp Ala  
50 55 60  
Arg Leu Ala Asp Tyr Phe Asp Val Ile Gly Gly Thr Ser Thr Gly Gly  
65 70 75 80  
Leu Leu Thr Ala Met Ile Ser Thr Pro Asn Glu Asn Asn Arg Pro Phe  
85 90 95  
Ala Ala Ala Lys Glu Ile Val Pro Phe Tyr Phe Glu His Gly Pro Gln  
100 105 110  
Ile Phe Asn Pro Ser Gly Gln Ile Leu Gly Pro Lys Tyr Asp Gly Lys  
115 120 125  
Tyr Leu Met Gln Val Leu Gln Glu Lys Leu Gly Glu Thr Arg Val His  
130 135 140  
Gln Ala Leu Thr Glu Val Val Ile Ser Ser Phe Asp Ile Lys Thr Asn  
145 150 155 160  
Lys Pro Val Ile Phe Thr Lys Ser Asn Leu Ala Asn Ser Pro Glu Leu  
165 170 175  
Asp Ala Lys Met Tyr Asp Ile Ser Tyr Ser Thr Ala Ala Ala Pro Thr  
180 185 190  
Tyr Phe Pro Pro His Tyr Phe Val Thr Asn Thr Ser Asn Gly Asp Glu  
195 200 205  
Tyr Glu Phe Asn Leu Val Asp Gly Ala Val Ala Thr Val Ala Asp Pro  
210 215 220  
Ala Leu Leu Ser Ile Ser Val Ala Thr Arg Leu Ala Gln Lys Asp Pro  
225 230 235 240



Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val  
 65 70 75 80  
 Ser Leu Glu Lys Arg Glu Ala Glu Ala Gln Leu Gly Glu Met Val Thr  
 85 90 95  
 Val Leu Ser Ile Asp Gly Gly Gly Ile Arg Gly Ile Ile Pro Ala Thr  
 100 105 110  
 Ile Leu Glu Phe Leu Glu Gly Gln Leu Gln Glu Met Asp Asn Asn Ala  
 115 120 125  
 Asp Ala Arg Leu Ala Asp Tyr Phe Asp Val Ile Gly Gly Thr Ser Thr  
 130 135 140  
 Gly Gly Leu Leu Thr Ala Met Ile Ser Thr Pro Asn Glu Asn Asn Arg  
 145 150 155 160  
 Pro Phe Ala Ala Ala Lys Glu Ile Val Pro Phe Tyr Phe Glu His Gly  
 165 170 175  
 Pro Gln Ile Phe Asn Pro Ser Gly Gln Ile Leu Gly Pro Lys Tyr Asp  
 180 185 190  
 Gly Lys Tyr Leu Met Gln Val Leu Gln Glu Lys Leu Gly Glu Thr Arg  
 195 200 205  
 Val His Gln Ala Leu Thr Glu Val Val Ile Ser Ser Phe Asp Ile Lys  
 210 215 220  
 Thr Asn Lys Pro Val Ile Phe Thr Lys Ser Asn Leu Ala Asn Ser Pro  
 225 230 235 240  
 Glu Leu Asp Ala Lys Met Tyr Asp Ile Ser Tyr Ser Thr Ala Ala Ala  
 245 250 255  
 Pro Thr Tyr Phe Pro Pro His Tyr Phe Val Thr Asn Thr Ser Asn Gly  
 260 265 270  
 Asp Glu Tyr Glu Phe Asn Leu Val Asp Gly Ala Val Ala Thr Val Ala  
 275 280 285  
 Asp Pro Ala Leu Leu Ser Ile Ser Val Ala Thr Arg Leu Ala Gln Lys  
 290 295 300  
 Asp Pro Ala Phe Ala Ser Ile Arg Ser Leu Asn Tyr Lys Lys Met Leu  
 305 310 315 320  
 Leu Leu Ser Leu Gly Thr Gly Thr Thr Ser Glu Phe Asp Lys Thr Tyr  
 325 330 335  
 Thr Ala Lys Glu Ala Ala Thr Trp Thr Ala Val His Trp Met Leu Val  
 340 345 350  
 Ile Gln Lys Met Thr Asp Ala Ala Ser Ser Tyr Met Thr Asp Tyr Tyr  
 355 360 365  
 Leu Ser Thr Ala Phe Gln Ala Leu Asp Ser Lys Asn Asn Tyr Leu Arg  
 370 375 380  
 Val Gln Glu Asn Ala Leu Thr Gly Thr Thr Thr Glu Met Asp Asp Ala  
 385 390 395 400  
 Ser Glu Ala Asn Met Glu Leu Leu Val Gln Val Gly Glu Asn Leu Leu  
 405 410 415



Lys Lys Pro Val Ser Glu Asp Asn Pro Glu Thr Tyr Glu Glu Ala Leu  
 420 425 430

Lys Arg Phe Ala Lys Leu Leu Ser Asp Arg Lys Lys Leu Arg Ala Asn  
 435 440 445

Lys Ala Ser Tyr  
 450

<210> 41

<211> 367

<212> PRT

<213> synthetic

<220>

<221> Protein

<222> (1)..(367)

<223> Post-cleavage patatin protein produced in Pichia pastoris

<400> 41

Glu Ala Glu Ala Gln Leu Gly Glu Met Val Thr Val Leu Ser Ile Asp  
 1 5 10 15

Gly Gly Gly Ile Arg Gly Ile Ile Pro Ala Thr Ile Leu Glu Phe Leu  
 20 25 30

Glu Gly Gln Leu Gln Glu Met Asp Asn Asn Ala Asp Ala Arg Leu Ala  
 35 40 45

Asp Tyr Phe Asp Val Ile Gly Gly Thr Ser Thr Gly Gly Leu Leu Thr  
 50 55 60

Ala Met Ile Ser Thr Pro Asn Glu Asn Asn Arg Pro Phe Ala Ala Ala  
 65 70 75 80

Lys Glu Ile Val Pro Phe Tyr Phe Glu His Gly Pro Gln Ile Phe Asn  
 85 90 95

Pro Ser Gly Gln Ile Leu Gly Pro Lys Tyr Asp Gly Lys Tyr Leu Met  
 100 105 110

Gln Val Leu Gln Glu Lys Leu Gly Glu Thr Arg Val His Gln Ala Leu  
 115 120 125

Thr Glu Val Val Ile Ser Ser Phe Asp Ile Lys Thr Asn Lys Pro Val  
 130 135 140

Ile Phe Thr Lys Ser Asn Leu Ala Asn Ser Pro Glu Leu Asp Ala Lys  
 145 150 155 160

Met Tyr Asp Ile Ser Tyr Ser Thr Ala Ala Ala Pro Thr Tyr Phe Pro  
 165 170 175

Pro	His	Tyr	Phe	Val	Thr	Asn	Thr	Ser	Asn	Gly	Asp	Glu	Tyr	Glu	Phe
			180					185					190		
Asn	Leu	Val	Asp	Gly	Ala	Val	Ala	Thr	Val	Ala	Asp	Pro	Ala	Leu	Leu
		195					200					205			
Ser	Ile	Ser	Val	Ala	Thr	Arg	Leu	Ala	Gln	Lys	Asp	Pro	Ala	Phe	Ala
	210					215					220				
Ser	Ile	Arg	Ser	Leu	Asn	Tyr	Lys	Lys	Met	Leu	Leu	Leu	Ser	Leu	Gly
225					230					235					240
Thr	Gly	Thr	Thr	Ser	Glu	Phe	Asp	Lys	Thr	Tyr	Thr	Ala	Lys	Glu	Ala
				245					250					255	
Ala	Thr	Trp	Thr	Ala	Val	His	Trp	Met	Leu	Val	Ile	Gln	Lys	Met	Thr
			260					265					270		
Asp	Ala	Ala	Ser	Ser	Tyr	Met	Thr	Asp	Tyr	Tyr	Leu	Ser	Thr	Ala	Phe
		275					280					285			
Gln	Ala	Leu	Asp	Ser	Lys	Asn	Asn	Tyr	Leu	Arg	Val	Gln	Glu	Asn	Ala
	290					295					300				
Leu	Thr	Gly	Thr	Thr	Thr	Glu	Met	Asp	Asp	Ala	Ser	Glu	Ala	Asn	Met
305					310					315					320
Glu	Leu	Leu	Val	Gln	Val	Gly	Glu	Asn	Leu	Leu	Lys	Lys	Pro	Val	Ser
			325						330					335	
Glu	Asp	Asn	Pro	Glu	Thr	Tyr	Glu	Glu	Ala	Leu	Lys	Arg	Phe	Ala	Lys
			340					345					350		
Leu	Leu	Ser	Asp	Arg	Lys	Lys	Leu	Arg	Ala	Asn	Lys	Ala	Ser	Tyr	
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<211> 7

<212> PRT

<213> synthetic

<220>

<221> Protein

<222> (1)..(7)

<223> Xaa3 = Phe, Ile, or Leu; Xaa5 = His or Asn

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Phe	Tyr	Xaa	Glu	Xaa	Gly	Pro
1				5		

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<211> 55

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55

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<211> 42

<212> DNA

<213> synthetic

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<222> (1)..(42)

<223> oligonucleotide-4

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42

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<211> 36

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<213> synthetic

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<223> oligonucleotide-5

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36

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39

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<210> 51

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<222> (1)..(55)

<223> oligonucleotide-11

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<210> 52

<211> 39

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<223> oligonucleotide-12

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39

<210> 53

<211> 55

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<222> (1)..(55)

<223> oligonucleotide-13

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<210> 54

<211> 39

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<222> (1)..(39)

<223> oligonucleotide-14

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<223> oligonucleotide-18

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39

<210> 59

<211> 55

<212> DNA

<213> synthetic

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55

<210> 60

<211> 39

<212> DNA

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<223> oligonucleotide-20

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39